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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - protein search, using sw model
                                                                                 Database :
                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            June 18, 2002, 11:43:07; Search time 19.66 Seconds (without alignments) 1055.712 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-454-651B-23
1149
                                                                                                                                                                                                                                                                                                          283138 seqs, 96089334 residues
                                                                                                                                                                                                                                                                                                                                                                                                               1 GLSHFCSGVIHVTKEVKEVA.....LRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                        283138
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	<u> </u>	DB	ID	Description
1	1149	100.0	288	2	A45803	cell-restri
2	1085		289	N	G00031	т.
ω	738		299	ν	I46690	rso
4	601.5		321	2	I54766	
5	561	8	309	N	I49503	ymphocyte
6	185		275	N	JC7604	CD86 spliced varia
7	182	15.8	329	ب	A48754	B7-2 antigen - hum
æ	152		309	ν	I49522	
9	140.5		330	Ν	I46691	precu
10	133.5	11.6	583	N	I39428	alcam - human
11	129		221	Н	QQBE48	BARF1 protein - hu
12	127	٠	526	Ν	S70587	butyrophilin precu
13	122.5	٠	588	Ν	JH0506	
14	122.5	10.7	588	N	A45254	race grycopro
15	120.5		509	ν,	JC5288	substrate-1
16	120.5	10.5	513	Ν	JC5289	
17	118	10.3	487	N	865133	philin - mo
18	116.5	10.1	1088	ب	IJXLNL	cell adhes
19	115		761	Н	IJHUNG	cell adhes
20	112.5		725	N	JE0099	Се
21	110.5	9.6	587	2	JH0464	RASP prec
22	109.5	9.5	646	N	I38049	e glyc
23	109.5	9.5	853	<u> </u>	IJBONC	Ω
24	109	9.5	526	N	A37821	butyrophilin - bov
25	109	9.5	2029	1	TDFFLK	tyrosine-
26	108	9.4	871	1	148696	tyrosine
27	108	9.4	881	Н	I48697	protein-tyrosine k
28	107.5	9.4	5175	2	T20992	hypothetical prote
29	107.5	9.4	5198	2	T43290	hemicentin precurs

45	44	43	42	41	40	39	38 8	37	36	<u>3</u> 5	34	ω ω	32	31	30
101	102	102.5	103	103	103.5	103.5	103.5	104	104	104	104.5	105.5	106	106.5	106.5
8.8	8.9	8.9	9.0	9.0	9.0	9.0	9.0	9.1	9.1	9.1	9.1	9.2	9.2	9. 3	9.3
1033	1443	503	1273	423	1115	725	480	1092	725	307	210	1091	267	858	333
2	N	N	Ν	N	ш	Н	N	Н	N	<u>-</u>	N	سر	Ν	\vdash	2
S19247	150600	JC5287	T42405	T29549	IJMSNL	IJMSNG	A56182	JN0635	JE0100	RWMSBC	A56169	IJCHNL	PL0064	IJRTNC	A31923
cell adhesion prot	neogenin - chicken	SHP substrate-1 pr	sax-3 protein - Ca	hypothetical prote	neural cell adhesi	neural cell adhesi	fibroblast growth	neural cell adhesi	neural cell adhesi	T-cell receptor be	Ig kappa chain V r	neural cell adhesi	T-cell receptor be	neural cell adhesi	amalgam protein pr

ALIGNMENTS

B-cell-restricted antigen B7 precursor - human
N;Alternate names: B-lymphocyte activation antigen B7
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Sep-1999
C;Accession: 154495; A45803
R;Selvakumar, A.; Mohanraj, B.K.; Eddy, R.L.; Shows, T.B.; White, P.C.; Dupont, B. Immunogenetics 36, 175-181, 1992
A;Ritle: Genomic organization and chromosomal location of the human gene encoding the A;Reference number: 154495; MUID:92307753
A;Accession: 154495

QY 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHPPDN 216	OY 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSODPETELYAVSSKLDF 180	Qy 61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120	Qy 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKWVLTMMSGDMNIWPE 60 	Query Match 100.0%; Score 1149; DB 2; Length 288; Best Local Similarity 100.0%; Pred. No. 2.1e-85; Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	A; Accession: L3437 A; Status: translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-288 < RES> A; Cross-references: GB:M83077; NID:g179327; PIDN:AAA58390.1; PID:g179329 A; Title: B7, a new member of the Ig superfamily with unique expression on activated a A; Reference number: A45803; MUID:90010147 A; Recession: A45803 A; Molecule type: mRNA A; Residues: 1-288 < CRES A; Cross-references: GB:M27533; NID:g184680; PIDN:AAA36045.1; PID:g306916 C; Genetics: A; Genetics: A; Genetics: GDB:CD80; CD28LG1; CD28 A; Cross-references: GDB:251792; OMIM:112203 A; Map position: 34/1; 140/1; 234/1; 266/1 C; Superfamily: B-lymphocyte restricted antigen B7 C; Keywords: transmembrane protein F; 1-6/Domain: Signal sequence #status predicted < MM> F; 248-264/Domain: transmembrane #status predicted < MM>

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CD80 precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999
C;Accession: I46690
R;Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
Immunogenetics 42, 217-220, 1995
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                                                                                                                                                                                                                                                                                                                                                            A;Reference number: I46689; MUID:95369849
A;Accession: I46690
                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Cloning and sequencing of the rabbit gene encoding A; Reference number: I46689; MITTD: 95360840
                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-299 <ISO>
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C:Species: Cercocebus torquatus (red-crowned mangabey, white-collared mangabey)
C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 29-Sep-1999
C:Accession: G00031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-289 <VIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: G00217
A; Accession: G00031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Villinger, F.J. submitted to the EMBL_Data Library, January 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U19833; NID:g644783; PIDN:AAA86700.1; PID:g644784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
      89
                                                                                                                                                                                  Local Similarity
                      64 RTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISD 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
                                                                                                                          4
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mes 205; Conservative
HFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKN 63
                                                                            HFSSGISQVTKSVKEMAALSCDYNISIDELARMRIYWQKDQQMVLSIISGQVEVWPEYKN 88
                                                                                                                                                                 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYCQKEKKMVLTMISGDMNIWPEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 61
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                                                                                                                                                               Conservative
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95.3%;
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63.9%;
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                                                                                                                                                                              Score 738; DB 2;
Pred. No. 3.3e-52;
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                                                                                                                                                           Mismatches
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                                                                                                                                                             39;
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R; Freeman, G.J.; Gray, G.S.; Gir
J. Exp. Med. 174, 625-631, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: MB7-2
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C;Accession: I49503; S17291; I49521
R;Selvakumar, A.; White, P.C.; Dupont, B.
Immunogenetics 38, 292-295, 1993
                                                                                                A;Title: Structure, expression, and T cell costimulatory activity of the murine homol A;Reference number: S17291; MUID:91341422
A;Accession: S17291
                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-309 <RES>
A;Cross-references: GB:L12589; NID:g293299; PIDN:AAA37240.1; PID:g293301
                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Genomic organization of the murine B-lymphocyte activation antigen A;Reference number: I49503; MUID:93307789
A;Accession: I49503
                                    A; Molecule type: mRNA
A; Residues: 1-274,'R',279-309 <FRE>
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A;Residues: 1-321 <RES
A;Cross-references: EMBL:U05593; NID:9453381; PIDN:AAA80154.1; PID:9453382
C;Superfamily: B-lymphocyte restricted antigen B7
A;Cross-references: EMBL:X60958; NID:g50111; PIDN:CAA43291.1; PID:g50112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B-lymphocyte activation antigen 7 precursor - mouse
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R;Judge, T.A.; Liu, M.; Christensen, P.J.; Fak, J.J.; Turka, L.A.
Int. Immunol. 7, 171-178, 1995
A;Title: Cloning the rat homolog of the CD28/CTLA-4-ligand B7-1: structural and funct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: I54766; MUID: 95252184
A; Accession: I54766
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C;Accession: I54766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 NITEYGNPSADIKRITCFASGGFPKPRLSWLENGRELNGINTTISQDPESELYTISSQLD 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 SISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 NNHSIVCLIKYGELSVSQIFPWSKPKQE 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 KYKNRTYYDIANNYSFSLLGLILSDRGTYTCVVQRYEGGSYVVKHLTTVELSVRADFPTP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 GLLQISSGIVGQVSKSVREKALLSCDYKFCSEEQSIHRIYWQKHDKMVLSVISGVPEVWP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FNATYDHFIDCFIEYGDAHVSQNFTW 236
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                                                                                                                                                                                                                    C.D.; Lombard, D.B.; Zhou, L.J.; White, M.; Finge
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R; Inobe, M.; Linsley, P.S.; Ledbetter, J.A.; Nagai, Y.; Tamakoshi, M.; Uede, T.
Biochem. Biophys. Res. Commun. 200, 443-449, 1994
A;Title: Identification of an alternatively spliced form of the murine homologue of B7.
A;Reference number: I49521; MUID:94220123
A;Recession: I49521 MUID:94220123
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-143,238-274,'R',279-309 <RE2>
A;Cross-references: GB:D16220; NID:9505118; PIDN:BAA03748.1; PID:9994769
C;Genetics:
A;Gene: B7
A,Intercor. 3771. 13371. 2377. 27574
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C;Superfamily: B-lymphocyte restricted antigen
C;Keywords: alternative splicing
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A;Residues: 1-275 <MAG>
C;Comment: This CD86 variant expressed by activated
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A;Title: Identification of an alternatively spliced variant of human CD86 mRNA.
A;Reference number: JC7604; MUID:21092744; PMID:11162656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
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C; Keywords: immune response
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 KRITCFASGGFPKPRFSWLENGRELPGINTTISQDPESELYTISSQLDENTTRNHTIKCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 RRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSFMCL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 TYSLIILGLVLSDRGTYSCVVQKKERGTYEVKHLALVKLSIKADFSTPNITESGNPSADT 160
     176 SKLDF---NMTTNHSFMCLIKYGHLRVNQ---TFNWNTTKQE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 LSKSVKDKVLLPCRYNSPHEDESEDRIYWOKHDKVVLSVIAGKLKVWPEYKNRTLYDNT- 100
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                                                                                                                                              84 SDSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRIHQMNSELSVLANFSQPEI----VPIS 139
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                                                                                                                                                                                         TNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTS 129
                                                                                                                                                                                                                                           ETADLPCQFANSQNQSLSELV---VFWQDQENLVLNEVYLGKEKFDSVHSKYMGRTSFD- 83
                                                                                                                                                                                                                                                                       EVATLSC----GHNVSVEELAQTRIYWQKEKKMVLTMM----SGDMNIWPEYKNRTIFDI 69
                                                NITENVYINLTCSSIHGYPEPKKMSVL-----LRTKNSTIEYDGIMQKSQDNVTELYDVS
                                                                                           NIR-----SQDPETELYAVS 175
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50.7%; Pred. No. 6.6e-38;
tive 41; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                              16.1%; Score 185; DB 2; 27.4%; Pred. No. 1.3e-07;
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                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                            78;
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R;Freeman, G.J.; Gribben, J.G.; Boussiotis, V.A.; Ng, J.W.; Restivo Jr., V.A.; Lombar Science 262, 909-911, 1993
A;Title: Cloning of Br-2: a CTLA-4 counter-receptor that costimulates human T cell pr A;Reference number: A48754; MUID:94053735
A;Accession: A48754
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               R;Freeman, G.J.; Borriello, F.; Hodes, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Kim J. Exp. Med. 178, 2185-2192, 1993
A;Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell A;Reference number: I49522; MUID:94065585
A;Accession: I49522
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A48754; S39055
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A;Map position: 3q13.3-3q21
C;Superfamily: B7-2 antigen
C;Keywords: glycoprotein
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A;Accession: S39055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:L25259; NID:g416368; PIDN:AAA58389.1; PID:g416369 A;Note: it is uncertain whether Met-1 or Met-7 is the initiator R;Azuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L. Nature 366, 76-79, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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                                                                                                                                                                                                      gene B7-2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
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A; Residues: 7-329 <AZU>
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A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 NIR-----RIICSTSGGFPEP-HLSWLENGEELNAINTTV------SQDPETELYAVS 175
                                                                                                                                                                                                                                                                                                                                                                                                                201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 SDSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRIHQMNSELSVLANFSQPEI----VPIS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 ETADLPCQFANSQNQSLSELV---VFWQDQENLVLNEVYLGKEKFDSVHSKYMGRTSFD- 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 EVATLSC----GHNVSVEELAQTRIYWQKEKKMVLTMM----SGDMNIWPEYKNRTIFDI 69
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60; Conserv
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Pred. No. 2.7e-07;
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Somoza,

10;

A; Molecule type: mRNA A; Residues: 1-309 < RES>

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alcam - human (man) (C;Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000 (C;Accession: I39428 (R;Bowen, M.A.; Patel, D.D.; Lt, X.; Modrell, B.; Malacko, A.R.; Wang, W.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: I46691
C;Accession: T46691
R;Isono, T:; Seto, A.
Immunogenetics 42, 217-220, 1995
A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecul A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecul A;Accession: I46689; MUID:95369849
A;Accession: I46691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 23-Jul-1999
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C;Superfamily: B7-2 antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                               177 KLDF-NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFP 214
                                                                                                                                                                                                                                                                                                                                                   132 RR-----SQDPETELY--AVSS 176
                                                                                                                                                                                                                            204 SITFSDDIRNATIYCVL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 GVWHMTVVCVLETESMKIS 226
                                                                                                                                                                                                                                                                                                                                                                                              94 NLQLHNVQIK--DKGVYQCFVHHRGAKGLVPIYQMNSELSVLANFTQPEIT----LISNI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 EVATLSCGH-NVSVEELAQTRIYWQKEKKMVLTMM----SGDMNIWPEYKNRTIFDITN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90
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                                                                                                                                                                                                                                                                                                            TRNSAINLTCSSVQGYPEPKKMFF----VLKTENATTEYDGVIEKSQDNVTGLYNISISG
                                                                                                                                                                                                                                                                                                                                                                                                                                         NLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTADLPCQFTNSQSRSLSELVVFWQDQERLVLYELFLGREKPDNVDPKYIGRTSFDQESW 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGNSGINLTCTSKQGHPKPKKMYFLITNSTNEYGDNMQISQDNVTELFSISNSLSLSFPD 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSNIR-RIICSTSGGFPEPHLSW--LENGEELNAINTTVSQDPETELYAVSSKLDFNM-- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNNWTLRLHNVQIKDMGSYDCFIQKKPPTGSIILQQTLTE--LSVIANFSEPEIKLAQNV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNNLSIVILALRPSDEGTYECVVLKYEK--DAFKREHLAEVTLSVKADFPTPSISDFEIP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AYLPCPFTKAQNISLSELV---VFWQDQQKLVLYEHYLGTEKLDSVN--AKYLGRTSFD- 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -TTNHSFMCLIKYGHLRVN 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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26.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.2%; Score 140.5; DB 2; 27.4%; Pred. No. 0.00062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 152; DB 2; Length 309, Pred. No. 6.7e-05;
                                                                                                                                                                                                                            -QTESTETYSQ-HFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                          233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 330;
                      A.R.; Wang, W.C.; Marquardt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
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C.Species: human herpesvirus 4, Epstein-Barr virus
C.Species: human herpesvirus 4, Epstein-Barr virus
C.Date: 25-Peb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999
C.Accession: B43045; A03792; S33058
R.Bankler, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A.Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epste.
                                                                                                                                         RESULT 12
S70587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome A;Reference number: A03794; MUID:84270667 A;Contents: annotation; protein coding region C;Superfamily: human herpesvirus 4 BARF1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:V01555; NID:g59074; pIDN:CAA24809.1; pID:g1334917 R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; G Nature 310, 207-211, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-221 <BAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A93065; MUID:85035713
A;Accession: B43045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BARF1 protein - human herpesvirus 4 (strain B95-8)
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A; Residues: 1-583 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Exp. Med. 181, 2213-2220, 1995
A;Title: Cloning, mapping, and characterization of activated leukocyte-cell adhesion
A;Reference number: I39428; MUID:95279947
A;Accession: I39428
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local
                                                                                                                                                                                                                                                                                                    113 -KADFPTPSISDFEIPTSNIRRIICSTSGGFPEPHLSWL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 PVTQLYTMTSTLEYKTTKADIQMPFTCSVTY 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 PETELYAVSSKLDFNMT---TNHSFMCLIKY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134
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                                                                                                                                                                                                                                                                                                                                                          72 WPFRGFFDIHRSANTFFLVVTAANISHDGNYLCRMKLGETEVTKQEHLSVVKPLTLSVHS
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                                                                                                                                                                                                                                                                                                                                                                                                           YKNRTIFDI----TNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEV---TLSV-- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QAVTAFLGERVTLTS-----YWRRVSLGPEIEVSWFKLGPGEEQVLIGRMHHDV-IFIE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVATLSCGHNVSVEELAQTRIYWQK-----
                                                                                                                                                                                                                                                ERSQFP-----DFSVLT-----VTCTVNAFPHPHVQWL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSKPEIVSKALFLETEQLKKLGDCISEDSYPDGNITWYRNGKVLHPLEGAVVIIFKKEMD 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSISDFE-----IPTSNIRRI-ICSTSGGFPEPHLSWLENGEELNAINTTV-----SQD 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEYKOR -- LNLSENYTLSISNARISDEKRFVCMLVT-EDNVFEAPTIVKV-----FKQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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27.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 129; DB 1; Length 221; Pred. No. 0.0031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44;
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A:Molecule type: protein
A;Residues: 34-48 <TAN1>
C;Comment: This protein is uniquely and transiently expressed on C;Keywords: glycoprotein; transmembrane protein
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-588/Product: adhesion molecule SC1 #status predicted <ADH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adhesion molecule SC1 precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jul-2000
C;Accession: JH0506; ps0270
R;Tanaka, H.; Matsul, T.; Agata, A.; Tomura, M.; Kubota, I.; McFarland, K.C.;
Reuron 7, 535-545, 1991
A;Title: Molecular cloning and expression of a novel adhesion molecule, SC1.
A;Reference number: JH0506; MUID:92030150
A;Accession: JH0506; MUID:92030150
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A;TitLe: Cloning and sequence analysis of human butyrophilin reveals a potential receptor A;Reference number: S70587; MUID:96201696
A;Accession: S70587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-588 <TAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-526 <TAY>
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Best Local
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Best Local
                         199 NRSTGLFTMTSSLQYMPTKEDANAKFTCIVTY 230
                                                                 166
                                                                                                                                                119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 QENGEICLECTSVGWYPEPQVQWRTSKGEKFP--STSESRNPDEEGLFTVAASVIIRDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
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                                                                                                                                                                                        90
                                                                                                                                                                                                                        59 PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89
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                                                             DPETELYAVSSKLDFNMT---TNHSFMCLIKY 194
                                                                                                     PSQPEILHQADF-LETEKLKMLGECVVRDSYPEGNVTWYKNGRVLQPVEEVVVINLRKVE
                                                                                                                                         PS-----ISDFEIPTSNIRRI-ICSTSGGFPEPHLSWLENG-----EELNAINTTVSQ 165
                                                                                                                                                                                  PDYKDR--LSLSENYTLSIKNARISDEKRFVCMLVT-EDDVSEEPTVVKV-----FKQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKNVSCYIQ 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIAKGRVALRIRGVRVSDDGEYTCF---FREDGSYEEAL--VHLKVAALGSDPHIS-MQV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKEVATLSC--GHNVSVEELAQTRIYWQKEKKMVLTMMSG---DMNIWPEYKNRTIF--- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -DITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEI 126
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Pred. No. 0.0
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A;Gene:
A;Map po
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Yamao, T.; Matozaki, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioka, Biochem. Biophys. Res. Commun. 231, 61-67, 1997
B;Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localiza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHP substrate-1 protein, 509 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: A45254; S19202
R;Pourquie, O.; Corbel, C.; Le Caer, J.P.; Rossier, J.; Le Douarin, N.M. Proc. Natl. Acad. Sci. U.S.A. 89, 5261-5265, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         surface glycoprotein BEN precursor - chicken
c; Species: Gallus gallus (chicken)
C; Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jul-2000
C; Accession: A45254; S19202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-509 < YAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Contents: Brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession:
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A; Residues: 1-588 < POU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: X64301; NID: g63087;
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position: 2
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134 EIQSGGGTEVYVLAKPSPPEVSGPADRGIPDQKV-NFTCKSHGFSPRNITLKWFKDGQEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPT 118
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                                                                                                                                              TMMSGDMNIWPEYKNRTIFDIT--NNL--SIVILALRPSDEGTYECVVLKYEKDAFKREH 104
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                                              L-----AEVTLSVKADFPTPS-ISDFEIPTSNIRRIICSTSGGFPEP-HLSWLENGEEL 156
                                                                                                YSFTGEH---FPRVTN--VSDATKRNNMDFSIRISNVTPEDAGTYYCV--KFQKGPSEPDT 133
                                                                                                                                                                                                SCFCTGVTGKELKVTQPEKSVSVAAGDSTVLNC---TLTSLLPVGPIKWYRGVGQSRLLI 79
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39; Conserv
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25.7%;
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                                                                                                                                                                                                                                                                                                                     Score 120.5; DB Pred. No. 0.044;
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Db Qy

Search completed: June 18, 2002, 11:43:56 Job time: 49 sec

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Title:
Perfect score:
Sequence: OM protein - protein search, using sw model Database : Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Total number of hits satisfying chosen parameters: Searched: Run on: Scoring table: June 18, 2002, 11:43:57; Search time 11.96 Seconds (without alignments) 699.283 Million cell updates/sec 105224 seqs, 38719550 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 1 GLSHFCSGVIHVTKEVKEVA.....LRVNQTFNWNTTKQEHFPDN 216 US-09-454-651B-23 1149 SwissProt_40:* GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. 105224

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

33 33 33 33 33 33	Result No.
738 561 182 183.5 134.5 133.5 139.5 139.5 139.5 139.5 1109.5 1109.5 1109.5 1109.5 1109.5 1109.5 1109.5 1109.5 1109.5 1109.5 109.5 1109.5 1109.5	score
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ALIGNMENTS

RA R	RA R	RN RA RA RR	RESULT CD80_H ID CD AC P DT 0 DT 0 DT 0 DT 0 DT 0 CD
geroth J.D., Gribben J.G., Nadler L.M.; xpression, and T cell costimulatory activit gue of the human B lymphocyte activation ar 174:625-631(1991). ION. 403; PubMed=7527824; 603; Pallon S., Somoza C., Phillips J.H., Lins to D., Azuma M.; d CD86 (B70) provide similar costimulatory ation, cytokine production, and generation 54:97-105(1995). LOGRAPHY (3.0 ANGSTROMS) OF 35-234. 11bert R.J., Fennelly J.A., Collins A.V., I ttuart D.I., Davis S.J.; ttuart D.I., Davis S.J.; 1-60(2000). INVOLVED IN THE COSTIMULATORY SIGNAL ESSEI ES ACTIVATION. T CELL PROLIFERATION AND CY.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=92307753; PubMed=1377173; MEDLINE=92307753; PubMed=1377173; MEDLINE=92307753; PubMed=1377173; Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C., Dupont B.; "Genomic organization and chromosomal location of the human gene encoding the B-lymphocyte activation antigen B7."; "Genomic organization and chromosomal location of the human gene encoding the B-lymphocyte activation antigen B7."; Immunogenetics 36:175-181(1992). [3] SEQUENCE OF 35-38. MEDLINE=91341422; PubMed=1714935; Freeman G.J., Gray G.S., Gimmi C.D., Lombard D.B., Zhou LJ.,	Primates; Catarrhini; Hominidae; ubMed=2794510; man A.S., Segil J.M., Lee G., Whi f the Ig superfamily with unique astic B cells."; 4-2722(1989).	LIT 1 _HUMAN _HUMAN CD80_HUMAN STANDARD; PRT; 288 AA. P33681; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) 11-MAR-2002 (Rel. 41, Last annotation update) 12-Mar-2003 (Rel. 41, Last annotation update) 13-Mar-2004 (Rel. 28, Craniate) 14-Mar-2004 (Rel. 28, Craniate) 15-Mar-2004 (Rel. 28, Craniate) 16-Mar-2004 (Rel. 28, Craniate) 17-Mar-2004 (Rel. 28, Craniate) 18-Mar-2004 (Rel. 28,

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207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND DENDRITIC CELLS.
-I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY
                   181
                                                         147
                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute.
                                                                                                                                   87
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                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEPTOR.
SUBCELLULAR LOCATION:
TISSUE SPECIFICITY: E:
                                                 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                       GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
               NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                             YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS
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216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M27533; AAA36045.1; -. M83077; AAA58390.1; -. M83072; AAA58390.1; JOJ M83073; AAA58390.1; JOJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M83074; AAA58390.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pean Bioinformatics Institute. There are no rest non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                    288 AA;
                                                                                                                                                                                                                                                                                      Conservative
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IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED
                                                                                                                                                                                                                                                                                  Score 1149; DB 1;
Pred. No. 3.5e-89;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                BA453EE34528B1F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Signal; Transmembrane;
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Query Match Best Local Similarity Matches 133;

64.2%;

Score 738 Pred. No.

.9e-55; DB

Length 299; Indels

Conservative

36;

Mismatches 738;

39;

0; Gaps

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TAGE CONSTRUCTION OF THE PROPERTY OF THE PROPE
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CD80_RABIT
                            CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD80_RABIT
P42070;
01-NOV-1995
01-NOV-1995
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                    CARBOHYD
                                                                                                                                                            CARBOHYD
                                                                                   CARBOHYD
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                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                           DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D49843; BAA08643.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenetics 42:217-220(1995).
-i- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 costimulatory molecules."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-B/J X CHBB:HM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
T lymphocyte activation antigen CD80 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning and sequencing of the rabbit gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Lagomorpha; Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isono T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00409; IG; 1.
SM00410; IG_like;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR003599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain;
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RESULT 3
CD80_MOUSE
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01-FEB-1994 (Rel. 28, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
T lymphocyte activation anticon conc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-91341422; PubMed-1714935; Gray G.S., Freeman G.J., Gimmi C.D., Lombard D.B., Zhou L.J., White M., Fingeroth J.D., Gribben J.G., Nadler L.M.; White M., Fingeroth J.D., Gribben J.G., Nadler L.M.; This is a structure, expression, and T cell costimulatory activity of the murine homologue of the human B lymphocyte activation antigen B7 J. Exp. Med. 174:625-631(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen) (B7).
CD80 OR B7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q00609;
01-FEB-1994
                        between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There are use by non-profit institutions as it modified and this statement is not removed. Usa entities requires a license agreement (See http: or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD80_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. TISSUE=B-cell;
                                                                                                                                                                                                                                                                                                                                                 Immunogenetics 38:292-295(1993).

-i- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Selvakumar A., White P.C., Dupont E
"Genomic organization of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93307789; PubMed=7686531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29
                                                                                                                                                            ACTIVATION. PROTEIN WAS DETECTED AT CELL SURFACE AT 24 HOURS AND IT'S EXPRESSION WAS MAXIMAL FROM 48 TO 72 HOURS POST-ACTIVATION. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN. SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Type I membrane protein. TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS,
                                                                                                                                                                                                                                                DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS
                                                                                                                                                                                                                                                                  MALIGNANCIES
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                                                                                                                                                                                                                                                                                    INTERFERON STIMULATED MONOCYTES AND NONCIRCULATING
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                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration
X60958; CAA43291.1;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dupont B.;
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Sciurognathi; Muridae;
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                                               (See http://www.isb-sib.ch/announce/
                                                                               There are no restrictions ng as its content is in
                                                               Usage
                                                                                                              and the
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; Murinae; Mus
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InterPro; IPR003006; Ig_MHC
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                SEQUENCE FROM N.A.
MEDLINE=94053735; PubMed=7694363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mmunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;; L12589; AAA37240.1; ;
,; L12585; AAA37240.1; ;
,; L12586; AAA37240.1; ;
,; L12587; AAA37240.1; ;
,; L12588; AAA37240.1; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S17291; S17291.
MGI:101775; Cd80.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSKSVKDKVLLPCRYNSPHEDESEDRIYWQKHDKVVLSVIAGKLKVWPEYKNRTLYDNT- 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSFMCL 191
                                                                                                                                                                                                                                                                                                                                                         IKYGDAHVSEDFTWEKPPEDP-PDS
                                                                                                                                                                                                                                                                                                                                                                                         IKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                                                              KRITCFASGGFPKPRFSWLENGRELPGINTTISQDPESELYTISSQLDFNTTRNHTIKCL
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SM00410; IG_like; 1
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N-LINKED
N-LINKED
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Pred. No. 5.9e-40;
1; Mismatches 58
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                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYMPHOCYTE ACTIVATION ANTIGEN CD80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 306;
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Freeman G.J.,

Gribben

J.G.,

Boussiotis

V.A.,

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J.W

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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IG_Y; 1.
PROSITE; PS00290; IG_MHC; FALSE_NEG.
Immunoglobulin domain; T_cell; Glycoprotein; Signal; Transmembrane;
                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94348060; PubMed-7520767;
Engel P., Gribben J.G., Freeman G.J., Zhou L.J., Noz
Nadler L.M., Wakasa H., Tedder T.F.;
"The B7-2 (B70) costimulatory molecule expressed by
activated B lymphocytes is the CD86 differentiation
Blood 84:1402-1407(1994).
                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Okumura K., Ito D., Azuma M.;
"CD80 (B7) and CD86 (B70) provide similar cell proliferation, cytokine production, J. Immunol. 154:97-105(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION.
MEDLINE=95088403; PubMed=7527824;
Lanier L.L., O'Fallon S., Somoza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genomic organization of the gene coding for the costimulatory human B-lymphocyte antigen B7-2 (CD86).";
Immunogenetics 42:85-89(1995).
                                                                                                                                                                                                                                                   or send
                                                                                                                                                                                                                                                                 entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Green N.R., Gray G.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Restivo V.A. Jr., Lombard L.A., Gray G.S., Nadler L.M.; "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell proliferation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION AS CD86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jellis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Foreskin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "B70 antigen is a second ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Azuma M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95331831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 366:76-79(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94050123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 262:909-911(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 7-329 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 7-329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS, SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T CELLS WITHIN 24 HOURS AFTER ACTIVATION.

SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN. DATABASE: NAME-PROW; NOTE-CD guide CD86 entry;
                                                                                                                                                                                                                                                                                                                                                                      WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd86.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MONOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: EXPRESSED BY ACTIVATED
                                                                                                      601020;
                                                                                                                                                   U17717;
U17718;
                                                                                                                     U17719;
U17721;
                                                                                                                                                                                  L25259; AAA58389.1; -. U04343; AAB03814.1; -. U17722; AAA86473.1; -.
                                                                                                                                                                                                                                              s requires a license agreement (San email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ito D.,
                                                                                                                     AAA86473.1;
                                                                                                                                AAA86473.1; JOINED AAA86473.1; JOINED AAA86473.1; JOINED AAA86473.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                       BELONGS TO THE IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=7541777;
S.S., Rennert P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yagita K., Okumura
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                                                                                                                                  JOINED.
                                                                                                                     JOINED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borriello F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      κ.,
                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
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075144; Q9NRQ1; Q9HD18;
15-JUL-1999 (Rel. 38, Cr
16-OCT-2001 (Rel. 40, La
           Yoshinaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H., Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.; "Characterization of a new human B7-related protein: B7RP-1 is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation updato ICOS ligand precursor (B7 homolog 2) (B7-H2 (B7-related protein-1) (B7RP-1). ICOSL OR B7H2 OR B7RP1 OR KIAA0653.
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CONFLICT
SEQUENCE
                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE-Peripheral blood lymphocytes; MEDLINE-20465019; PubMed-11007762;
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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IG-LIKE C2-TYPE DOMAIN.
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Catarrhini;
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a B7-like molecule
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(B7-H2) (B7-like protein G150)
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RA LING V., DUNIESI-JOANNO, C.,

RY "GISO molecules and uses therefor.",

RL Patent number WO0121796, 29-MAR-2001.

RL Patent number WO0121796, 29-MAR-2001.

CC -!- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR

CC CYTOKINE SECRETION; DUNCES ALSO B-CELL PROLIFERATION AND

CC CYTOKINE SECRETION; DIAGNA CELLS. COULD PLAY AN IMPORTANT ROLE IN

CC CYTOKINE SECRETION; DIAGNA CELLS. COULD PLAY AN IMPORTANT ROLE IN

CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS

CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-

STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By Similarity).

CC -!- SUBCELLULAR DOCATION: Type I membrane protein (By Similarity).

CC -I- SUBCELLULAR LOCATION: Type I membrane protein (By Similarity).

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CC -I- SUBCE
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                            B-cell activation;
                                                  SMART;
                                                                        Interpro; 1.... 1g; 3. Pfam; PF00047; 1g; 3.
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DNA Res. 5:169-176(1998).
    Immunoglobulin domain;
                                                                                                                 InterPro; IPR003006;
InterPro; IPR003600;
                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification of GL50, a novel B7-like protein that functionally sinds to TCOS recentor.":
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                                                                                                                                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                           AF199028; AAF34739.1; -. AF289028; AAG01176.1; -. AF216749; AAK16241.1; -.
                                                                                                                                                                                                             SM00410; IG; 1.
SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                  an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                   requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                               IPR003599; Ig.
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Immune response; Glycoprotein;
in; Signal; Transmembrane; Mul
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Thomas J.L., Miyashiro J.S.,
Multigene family;
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Best Local S
Matches 57
                                                                                                                                                                                                                                                                                                                                                                                                          _MOUSE
                                                                                                                          Wang S., Gray G.S., Nadler L.M., Sharpe A.H.;
"Murine B7-2, an alternative CTLA4 counter-receptor that costimulates
T cell proliferation and interleukin 2 production.";
J. Exp. Med. 178:2185-2192(1993).
                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
VARSPLIC
SEQUENCE
                                  MEDLINE=96094437; PubMed=7499829;
Borriello F. Oliveros J., Freeman G.J
"Differential expression of alternate
J. Immunol. 155:5490-5497(1995).
                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
T lymphocyte activation antigen CD86 precursor (Activation B7-2 antigen) (Early T cell costimulatory molecule-1) (ETC-1).
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SEQUENCE OF 7-309
MEDLINE=94230971;
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Freeman G.J., Borriello F., Hodes R.J., Reiser H., (
Ng J.W., Kim J., Goldberg J.M., Hathcock K., Laszlo
                                                                                                                                                                                                                                                                                                                                                                                            CD86_MOUSE
                                                                                                     SEQUENCE FROM N.A.
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Pred. No. 1.7e-06;
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GHV -> ESWNLLLLLS (IN ISOFORM 2).
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IG-LIKE C2-TYPE DOMAIN.
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                                              G.J., Nadler L.M., ate mB7-2 transcrip
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o G., Lombard
                                                     Sharpe A.H.;
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Best Loc
Matches
                                                  Query Match
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EMBL; U39456; AAC52334.1; J
EMBL; U39461; AAC52334.1; J
EMBL; U39461; AAC52334.1; J
EMBL; U39462; AAC52334.1; J
EMBL; U39464; AAC52334.1; J
EMBL; U39465; AAC52334.1; J
EMBL; U39466; AAC52334.1; J
EMBL; U39466; AAC52334.1; J
EMBL; U39466; AAC52336.1; A\
EMBL; U39461; AAC52336.1; J
EMBL; U39462; AAC52336.1; J
EMBL; U39463; AAC52336.1; J
EMBL; U39464; AAC52336.1; J
EMBL; U39464; AAC52336.1; J
EMBL; U39464; AAC52336.1; J
EMBL; U39466; AAC52336.1; J
EMBL; U39466; AAC52336.1; J
EMBL; U39467; AAC52336.1; J
EMBL; U39468; AAC52336.1; J
EMBL; U39464; AAC52336.1; J
EMBL; U39466; AAC52336.1; J
EMBL; U39466; AAC52336.1; J
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EMBL; U39468; 
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"Molecular cloning and expression of early T cell costimulatory
molecule-1 and its characterization as B7-2 molecule.";

J. Immunol. 152:4939-4936(1994).

-I- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a light of the statement is not removed.
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           Local Similarity
nes 52; Conserv
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SUBCELLULAR LOCATION: Type I membrane protein.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-7 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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IPR003596; Ig_v.
13.2%; Score 152; DB 1; ilarity 26.1%; Pred. No. 9.9e-06; Conservative 43; Mismatchen 77
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AAC52336.1; JOINED.
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AAC52336.1; ALT_INIT
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main; T-cell; Glycoprotein; Signal; Transmembrane;
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               78;
                                                  Length 309;
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                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=C3H/HeJ; TISSUE-Fetal thymus;
MEDLINE-20126021; PubMed-10657606;
Ling V., Wu P.W., Finnerty H.F., Bean K.M., Sp.
Leonard J.P., Hunter S.E., Zollner R., Thomas
Jacobs K.A., Collins M.;
"Identification of GL50, a novel B7-like prote
binds to ICOS receptor.";
J. Immunol. 164:1653-1657(2000).
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2002 (Rel. 41, Last annotation update)
1COS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein G150)
(B7-related protein 1) (B7RP-1) (LICOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yoshinaga S.K., Whorlskey J.S., Khare S.D., Sarmiento U., Guo J., Horan T., Shih G., Zhang M., Coccia M.A., Kohno T., Tafuri-Bladt A., Brankow D., Campbell P., Chang D., Chiu L., Dai T., Duncan G., Elliott G.S., Hui A., McCabe S.M., Scully S., Shahinian A., Shaklee C.L., Van G., Mak T.W., Senaldi G.; "T-cell co-stimulation through B7RP-1 and ICOS."; Nature 402:827-832(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Swallow M.M., Wallin J.J., Sha W.C.; "B7h, a novel costimulatory homolog of B7.1 and B7.2, is induced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Lymphocytes; MEDLINE=20083495; PubMed=10617205;
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                                                                                         variants: lymphoid
molecules.";
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SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
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                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rissue-Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                     Differential expression of inducible costimulator-ligand splice
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                                                                                                                                                                                                                  Wu P.W.,
                                                               166:7300-7308(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                  Miyashiro J.S., Marusic S., Finnerty H.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ISOFORM 1), AND CHARACTERIZATION
                                                                                                                         regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200
                                                                                                                                                                                                                                                                                                                                                                                                                                 a novel B7-like protein that functionally
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                     mouse g150-b and human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spaulding V., Fous
as J.L., Miyashiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
; Murinae; Mus
                                                                                                                         g150
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Ling V., Dunussi-Joannopolulos K.;

"GL50 molecules and uses therefor.";

Patent number WO121796, 29-MAR-2001.

-1- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR

CYTOKINE SECRETION; INDUCES ALSO H-CELL PROLIFERATION AND

DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN

MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS

WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-

STIMULATING MEMORY T CELL FUNCTION. DURING PREGNANCY, MAY FUNCTION

STEMPLATING MEMORY TO CELL FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                        B-cell activation; Immune response; Glycoprotein; Immunoglobulin domain; Signal; Transmembrane; Mul
                                                                                                                                                                                                                                                                                  SMART; SM00409; IG; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                         CARBOHYD
                                                      CARBOHYD
                                                                 CARBOHYD
                                                                                 CARBOHYD
                                                                                            DISULFID
                                                                                                          DISULFID
                                                                                                                                                                            DOMAIN
                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                              Alternative
                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                             InterPro; IPR003600; Ig_like
                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUES, SPECIFICITY: ISOFORM I HIGHEST EXPRESSION IN LYMPHOID TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NOD (PARTICULARLY IN THE CONTEX AND IN BOTH PRIMARY AND SECONDARY POLLICLES), THYMUS (PREDOMINANTLY IN THE MEDULLA) AND PEYER'S PATCHES (MOSTLY IN THE FOLLICLES), LOWER LEVELS IN MANY NONLYMPHOLD TISSUES, SUCH AS BRAIN, HEART, KIDNEY, LIVER, LUNG, SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC CELLS, T-CELLS, DENDRITIC CELLS AND ARCROPHAGES. THE EXPRESSION ISOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY.

DEVELOPMENTAL STAGE: DETECTED EARLY IN HEMOPOLESIS: IN THE YOLK SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type I membrane protein. ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TH2 PHENOTYPE
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AX100593;
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                                                                                                                                                                                                                                                                                                                                       IPR003599; Ig.
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; AAF34738.1; -.
; CAC36463.1; -.
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IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                         N-LINKED
                                                                                                                                                 CYTOPLASMIC (POTENTIAL). IG-LIKE V-TYPE DOMAIN. IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD86_RABIT
P42071;
01-NOV-1995
                                                                                                                                                                                                                                                                                  "Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecules.";
Immunogenetics 4:217-220(1995).
II FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTE PROLIFERATION AND INVERLEURIN 2 PRODUCTION, BY HINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS, SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
B lymphocyte activation antigen CD86 precursor (Activation B7-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen).
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                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95369849; PubMed=7642234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; 
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD86
                            InterPro; IPR003006;
InterPro; IPR003596;
                                                                                       or send
                                                                                                                      modified and this statement is not removed.
                                                                                                                                                  the
                                                                                                                                                                    between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9986;
                                                            EMBL; D49842; BAA08642.1;
                                                                                                                                                                                                                                                                                                                                                                                                             sono T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161
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                                                                                                                                                                                                            CELLS WITHIN 24 HOURS AFTER ACTIVATION.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
                                                                                                                                  European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYKSPGINVDSSYKNRGHLSLDSMKQGNFSLYLKNVTPQDTQEFTCRV--FMNTATELVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILEEVVRLRVAANFSTPVISTSDSSNPGQE-RTYTCMSKNGYPEPNLYWI-NTTDNSLID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cuniculus (Rabbit).
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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35960 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lagomorpha; Leporidae;
                         Ig_MHC.
Ig_v.
                                                                                                       license agreement (See http://www.isb-sib.ch/announce/
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27.1%;
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                                                                                                                      Usage
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PROSITE;

PS00290;

IG_MHC; 1

SM00406;

IGV;

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RESULT
C166_M
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Best Local :
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C166_MOUSE STAND...
Q61490; O70136;
Q61490; O70136;
Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1999 (Rel. 38, Last sequence update)
Q1-MAR-2002 (Rel. 41, Last annotation update)
Q1-MAR-2002 (Rel. 
                                                                                                                                                                                                                   MEDLINE-97353242; PubMed-9209500;
Bowen M.A., Bajorath J., D'Egidio M., Whitney G.S., Palmer D.,
Kobarg J., Starling G.C., Siaddak A.W., Aruffo A.;
"Characterization of mouse ALCAM (CD166); the CD6 binding domain
conserved in different homologs and mediates cross-species bindin
Eur. J. Immunol. 27:1469-1478(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
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DOMAIN
MEDLINE=94376084; PubMed=8089660;
Kanki J.P., Chang S., Kuwada J.Y.;
"The molecular cloning and characterization
DM-GRASP homologs in zebłafish and mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                   STRAIN-BALB/C; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                 OF 227-583 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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37142 MW;
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IG-LIKE C2-TYPE DOMAIN.
POTENTIAL.
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                            cross-species binding.";
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CONFLICT
CONFLICT
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EMBL; L25274;
HSSP; Q13740;
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CARBOHYD
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00409; IG; 3.
SMART; SM00410; IG_11ke;
PROSITE; PS00290; IG_MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003600; Ig_like
                                                                                                                                                                            SEQUENCE
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                    167
                                                             119
                                                                                                     59
                                                                                 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE NERVOUS SYSTEM.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: CELL ADHESION MOLECULE NEURITE EXTENSION BY NEURONS VIA INTERACTIONS. MAY PLAY A ROLE IN ACTIVATED LEUKOCYTES, AS WELL AS
PGTQLYTVTSSLEYKTTRSDIQMPFTCSVTY 224
                   PETELYAVSSKLDFNMTTNH---SFMCLIKY 194
                                                                               PEYKDR -- LSLSENYTLSIANAKISDEKREVCMLVT -EDNVFEAPTLVKV
                                                                                                  PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPT 118
                                                           PSISDFE----IPTSNIRRI-ICSTSGGFPEPHLSWLENGEELNAINTTVS----
                                        PSKPEIVNKAPFLETDQLKKLGDCISRDSYPDGNITWYRNGKVLQPVEGEVAILFKKEID
                                                                                                                                                                                                                                                                                                                                                                                                                          Signal
                                                                                                                                  Similarity
                                                                                                                                                                                                         157
270
270
354
4354
4354
4357
167
167
1487
489
                                                                                                                         Conservative
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AAA37528.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alcam.
                                                                                                                                                                                   65161
                                                                                                                                 11.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                              FALSE_NEG
                                                                                                                        34;
                                                                                                                                                                                           POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

IG-LIKE C2-TYPE DOMAIN 3.

POTENTIAL.
                                                                                                                                 Score 134.5;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                       CD166 ANTIGEN
                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                    domain; Glycoprotein; Transmembrane;
                                                                                                                                                                           E7BAFA8FCA8F9489
                                                                                                                       Mismatches
                                                                                                                                                                                    F (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THAT BINDS TO CD6. INVOLVED IN
HETEROPHILIC AND HOMOPHILIC
THE BINDING OF T AND B CELLS I
IN INTERACTIONS BETWEEN CELLS
                                                                                                                                  .00063;
                                                                                                                                           DB 1;
                                                                                                                        54;
                                                                                                                                                                                             (IN
                                                                                                                                                                         CRC64;
                                                                                                                                                                                           REF.
                                                                                                                                          Length
                                                                                                                        Indels
                                                                                                                                                                                                                                              (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                        25;
                                                                               -FKQ 133
                                                            ဗွ်
                                                                                                                       Gaps
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C166_HUMAN
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Q13740; O60892;

Q1-NOV-1997 (Rel. 35, Created)

Q1-NOV-1997 (Rel. 35, Last sequence update)

Q1-MAR-2002 (Rel. 41, Last annotation update)

CD166 antigen precursor (Activated leukocyte-cell adhesion molecule)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96420463; PubMed-8823162;
Skonier J.E., Bowen M.A., Emswiler J., Aruffo A., Bajorath J.;
"Recognition of diverse proteins by members of the immunoglobulin
superfamily: delineation of the receptor binding site in the human
CD6 ligand ALCAM.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Degen W.G., van Kempen L.C., Gijzen E.G., van Groningen J.J., van Kooyk Y., Bloemers H.P., Swart G.W.; "MEMD, a new cell adhesion molecule in metastasizing human melanoma cell lines, is identical to ALCAM (activated leukocyte cell adhesion molecule)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning, mapping, and characterization of adhesion molecule (ALCAM), a CD6 ligand."; J. Exp. Med. 181:2213-2220(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95279947; pubMed=7760007;
BOWEN M.A., Patel D.D., Li X., Modrell B., Malacko A.R.,
BOWEN M.A., Marquardt H., Neubauer M., Pesando J.M., Francke
Haynes B.F., Aruffo A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 2-583 FROM N.A. MEDLINE=98161527; PubMed=9502422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 35:12287-12291(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD6-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALCAM OR MEMD.
                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular model of the N-terminal receptor-binding domain human CD6 ligand ALCAM."; Protein Sci. 4:1644-1647(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bajorath J., Bowen M.A., Aruffo A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96060095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3D-STRUCTURE MODELING
                                                                                                                                                                                                                                                                     THE NERVOUS SYSTEM.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS
SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                             FUNCTION: CELL ADHESION MÓLECULE NEURITE EXTENSION BY NEURONS VIA INTERACTIONS. MAY PLAY A ROLE IN ACTIVATED LEUKOCYTES, AS WELL AS
                                                                                                                                                              European
                                                                                                                                                                                                                                     WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd166.htm".
                                                                                                                                                                                                                                                        DATABASE: NAME-PROW; NOTE-CD guide CD166 entry;
             L38608; AAB59499.1;
Y10183; CAA71256.1;
IKJC; 03-APR-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pathol. 152:805-813(1998).
                                                                                                                                           Bloinformatics Institute. The profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=8520490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (activated leukocyte cell adhesion
                                                                                                                                                                                                                                                                                                                                                                 THAT BINDS TO CD6. INVOLVED IN HETEROPHILIC AND HOMOPHILIC THE BINDING OF T AND B CELLS TO IN INTERACTIONS BETWEEN CELLS OF
                                                                                                                                           There are no restrictions ing as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activated leukocyte-cell
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ACC OCC OCC RN
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                                                                                                                                    BRF1_EBV
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                                                                                   21-JUL-1986
21-JUL-1986
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00409; IG; 2.
SMART; SM00410; IG_like; 2.
SMART; SM00410; IG_MHC; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPRUUJUVV, --
Pfam; PF00047; ig; 5.
Pfam; PM00409; IG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane; Repeat; Signal; 3D-structure; Polymorphism.
                                                                                                                BRF1_EBV 
P03228;
                                   Epstein-barr virus (strain B95-8) (Human herpesvirus Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
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MEDLINE=84270667;
          SEQUENCE FROM N.A.
                                                                   BARFI
                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                           NCBI_TaxID=10377;
                                                                           33 kDa early
                                                                                                                                                                                                               134
                                                                                                                                                                                             167
                                                                                                                                                                           194
                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                       PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPT 118
                                                                                                                                                                          PVTQLYTMTSTLEYKTTKADIQMPETCSVTY 224
                                                                                                                                                                                                               PSKPEIVSKALFLETEQLKKLGDCISEDSYPDGNITWYRNGKVLHPLEGAVVIIFKKEMD 193
                                                                                                                                                                                                                                                     PEYKDR--LNLSENYTLSISNARISDEKRFVCMLVT-EDNVFEAPTIVKV-----FKQ 133
                                                                                                                                                                                                                                 PSISDFE----IPTSNIRRI-ICSTSGGFPEPHLSWLENGEELNAINTTV--
                                                                                                                                                                                           PETELYAVSSKLDFNMT---TNHSFMCLIKY 194
                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR003599;
IPR003006;
                                                                                    (Rel. 01,
(Rel. 01,
(Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                               43
157
270
270
354
435
435
167
167
167
265
361
480
499
258
                                                                                                                                                                                                                                                                                           Conservative
                                                                           protein
                                                                                                                                                                                                                                                                                                                                          AΑ;
                                                                                                                            STANDARD;
 PubMed=6087149
                                                                                                                                                                                                                                                                                                                                          65132 MW;
                                                                          (p33).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig_like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig_MHC
                                                                                                                                                                                                                                                                                                     11.6%;
                                                                                    Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG-LIKE V-TYPE DOMAIN 1.
IG-LIKE V-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
POTENTIAL.
                                                                                                                                                                                                                                                                                                     Score 133.5; DB 1
Pred. No. 0.00077;
                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED
N -> S.
                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD166 ANTIGEN.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                          /FTId=VAR_003908.
E023FB3974A60284 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
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                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                            Mismatches
                                                                                    update)
on update)
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C2-TYPE DOMAIN 2.
C2-TYPE DOMAIN 3.
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(POTENTIAL)
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(POTENTIAL)
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BUTY_HUMAN
ID BUTY_HA
AC 013410
DT 01-NOV
DT 16-OCT
BUTYCO
GN BTN1A1
OS HOMO S
OC EUKARY
OC MAMMA1
ON NCBIT
RN [1]
RP SEQUEN
RX MEDLIN
RA TAYLOI
RT POTENT
RL BIOCHI
CC AK
CC MM
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                  BUTY_HUMAN STANDARD: PRT; 5
013410;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
            Taylor M.R., Peterson J.A., Ceriani R.L., Couto J.R.,
"Cloning and sequence analysis of human butyrophilin reveals a
potential receptor function.",
Biochim. Biophys. Acta 1306:1-4(1996).
-i- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS.
MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
                                                                                                                                                                                                                                                                         Butyrophilin precursor (BT). BTN1A1 OR BTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A03792; QQBE48.
PIR; S33058; S33058.
InterPro; IPR003600; Ig_like.
SMART; SM00410; IG_like; 1.
                                                                                                                                    MEDLINE=96201696; PubMed=8611614;
                                                                                                                                                     TISSUE=Breast;
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Early protein; Oncogene. SEQUENCE 221 AA; 24471 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; V01555; CAA24809.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90059873; PubMed=2555151; Wei M.X., Ooka T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBO J. 8:2897-2903(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 310:207-211(1984).
[2]
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Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C.,
Tuffnell P.S., Barrell B.G.;
"DNA sequence and expression of the B95-8 Epstein-Barı
                                                                                                                                                                                                                                                                                                                                                                                                                                                             132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A transforming function of the BARF1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 -KADEPTPSISDEEIPTSNIRRIICSTSGGFPEPHLSWL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION OF PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 WPFRGFFDIHRSANTFFLVVTAANISHDGNYLCRMKLGETEVTKQEHLSVVKPLTLSVHS
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   MEMBRANE (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QAVTAFLGERVTLTS-----YWRRVSLGPEIEVSWFKLGPGEEQVLIGRMHHDV-IFIE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                      Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                      Primates;
                                                                                                                                                                                                                                    Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.2%;
27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 129;
Pred. No. 0
                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA5A24D1EA28758E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                       update
                                                                                                                                                                                                                                                                                                                                                                       526 AA
                                                                                                                                                                                                                                                                                                    update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----EKKMVLTMMSGDMNIWPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Epstein-Barr virus genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 221;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Epstein-Barr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguin C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
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RESULT 13
C166_CHICK
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Best Local
                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
CD166 antigen precursor (SC1 glycoprotein) (B
GRASP protein) (JC7 protein).
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
DOMAIN
                                   Archosauria; Aves; Neognathae;
                                                  Eukaryota; Metazoa;
                                                                                                                                            P42292;
                                                                                                                                                        C166_CHICK
            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1.
Pfam; PF00622; SPRY; 1.
SMART; SM00406; IGV; 1.
SMART; SM00449; SPRY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Glycoprotein; SIGNAL 1 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                       16 VKEVATLSC--GHNVSVEELAQTRIYWQKEKKMVLTMMSG---DMNIWPEYKNRTIF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
                                                                                                                                                                                                                                                                        QENGEICLECTSVGWYPEPQVQWRTSKGEKFP--STSESRNPDEEGLFTVAASVIIRDTS
                                                                                                                                                                                                                                                                                                                           GIAKGRVALRIRGVRVSDDGEYTCF---FREDGSYEEAL--VHLKVAALGSDPHIS-MQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                 PTSNIRRIICSTSGGFPEPHLSW-LENGEELNAINTTVSQDPETE-LYAVSSKLDFNMTT 184
                                                                                                                                                                                                                                                                                                                                                  -DITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEI 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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IPR003596; Ig_v.
IPR003877; SPRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR003878;
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                                              Chordata; Craniata; Vertebrata; Euteleostomi;
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Ig_MHC.
Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPRY_domain
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CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

WHY E9ECAOCF8DAF94D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 127; DB 1; Pred. No. 0.0024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin domain; Signal.
BY SIMILARITY,
BUTYROPHILIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                        PRT;
                                   Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                     (BEN
                                  Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 526;
                                                                                     glycoprotein) (DM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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POUTQUIE O., Hallonet M.E.R., le Douarin N.M.;

Poutquie O., Hallonet M.E.R., le Douarin N.M.;

"Association of BEN glycoprotein expression with climbing fiber

axonogenesis in the avian cerebellum.";

J. Neurosci. 12:1548-1557(1992).

-I- FUNCTION: HOMOPHILIC ADBRESION MOLECULE ASSOCIATED WITH CLIMBIN

FIBER AXONOGENESIS. SUPPORTS NEURITE EXTENSION.

-I- SUBCELTULAR LOCATION: Type I membrane protein.

-I- TISSUE SPECIFICITY: EXPRESSED IN A RESTRICTED POPULATION OF A)

WITHIN THE SPINAL CORD IT IS LOCALIZED TO AXONS IN THE DORSAL

FUNICULUS, MIDLINE FLOOR PLATE CELLS, AND MOTONEURONS. FOUND

EPITHELIA, CENTRAL NERVOUS SYSTEM, AND HEMOPOIETIC CELLS. EACH

DEVELOPING SYSTEM CARRIES DIFFERENTLY GLYCOSYLATED MOLECULAR!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuron
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pourquie O., Corbel C., le Caer J.-P., Rossier J., "BEN, a surface glycoprotein of the immunoglobulin expressed in a variety of developing systems."; Proc. Natl. Acad. Sci. U.S.A. 89:5261-5265(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tanaka H., Matsui T., Agata A., Tomura M., Kubota I.,
McFarland K.C., Kohr B., Lee A., Phillips H.S., Shelton D.L.;
"Molecular cloning and expression of a novel adhesion molecule, SC1.";
 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92211411; PubMed=1313497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92302224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                that supports neurite e
Neuron 7:209-220(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burns F.R., von Kannen S., Chang S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91337449; PubMed=1873027;
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                                                                                                                                                                                 InterPro: IPR003599; Ig.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003600; Ig_like.
Pfam; PF00047; ig; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Bursa of fabricius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "DM-GRASP, a novel immunoglobulin superfamily
                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                        entities requires a
                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The European Bioinformatics Institutions as long
                                                             DOMAIN
                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS. SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF BEN.
DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVELOPMENT.
                                                                                                                          adhesion;
                                                                                                                                                                                                                                              $63276; AAB20170.1; -. M76678; AAA48602.1; -. X64301; CAA45579.1; -. Q13740; 1KJC.
                                                                                                                               SM00409; IG; 3.
SM00410; IG_like; 2.
SM00410; IG_MHC; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                        ed and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7:535-545(1991).
                                                                                                                                                                                                                                                                                                                           an
                                                                                                          Signal
                                                                                                                                                                                                                                                                                                                                                                   non-profit
                                                                                                                                                                                                                                                                                                                          equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                                        Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=1608932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STAGE: WIDELY EXPRESSED DURING EMBRYONIC
 588
532
588
126
233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                extension.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guy L.,
CD166 ANTIGEN.
EXTRACELLULAR (POTENTIAL POTENTIAL).
CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN 1.
IG-LIKE V-TYPE DOMAIN 2.
                                                                                                                       domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Raper
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                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                          Usage
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BUTY_
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Best Local
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BUTY_MOUSE
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15-JUL-1998 (Rel. 36, Last seq
16-OCT-2001 (Rel. 40, Last ann
Ishii T., Aoki N., Noda A., Adachi T., Nakamura R., Matsuda "Carboxy-terminal cytoplasmic domain of mouse butyrophilin specifically associates with a 150-kDa protein of mammary epecils and milk fat globule membrane.";
Biochim. Biophys. Acta 1245:285-292(1995).
                                                         TISSUE=Mammary gland;
MEDLINE=96125722; PubMed=8541302;
                                                                                                                   Ogg S.L., Komaragiri M.V.S., macues in Structural organization and mammary-specific
                                                                                                                                  STRAIN-129; TISSUE-Mammary gland; MEDLINE-97148936; PubMed-8995761; Ogg S.L., Komaragiri M.V.S., Math
                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                       Butyrophilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                 SEQUENCE
                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                              BTN1A1 OR BTN
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                                                                                                               butyrophilin
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                                                                                                                                                                                                                                                                                                                                                                  DPETELYAVSSKLDFNMT - - - TNHSFMCLIKY
                                                                                                                                                                                                                                                                                                                                                                                                                              PDYKDR--LSLSENYTLSIKNARISDEKRFVCMLVT-EDDVSEEPTVVKV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPT 118
                                                                                                                                                                                                                                                                                                                                                                                       PSQPEILHQADF-LETEKLKMLGECVVRDSYPEGNVTWYKNGRVLQPVEEVVVINLRKVE
                                                                                                                                                                                                                                                                                                                                                                                                        PS-----ISDFEIPTSNIRRI-ICSTSGGFPEPHLSWLENG-----EELNAINTTVSQ 165
                                                                                                   ophilin gene.";
Genome 7:900-905(1996).
                                                                                                                                                                                                                                                                                 P97392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                 OF 39-487 FROM N.A.
                                                                                                                                                                 FROM
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271
312
366
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352
433
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                                                                                                                                                                                                                                         precursor (BT).
                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.7%;
                                                                                                                                                                                                                                                 Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
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N-LINKED (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 122.5; DB 1;
Pred. No. 0.0064;
""scmatches 54;
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A -> S (IN REF. 3).
SD -> RH (IN REF. 3).
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IG-LIKE
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                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2A28612D0164531E CRC64;
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> RH (IN REF. 5).
'IN REF. 2).
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(GLCNAC.
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                               epithelial
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SECRETION OF MILK-FAT DROPLETS.

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Best Local
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Pfam; PF00622; SPRY; 1.
SMART; SM00406; IGY; 1.
SMART; SM00449; SPRY; 1.
Transmembrane; Glycoprotein; I.
SIGNAL 1 26
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CONFLICT
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CARBOHYD
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SUBGULT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN ASSOCIATION WITH THE MILK-FAT-CLOBULE MEMBRANE DURING LACTATION.

DEVELOPMENTAL STAGE: EXPRESSION INCREASES DURING THE LAST HALF OF PREGNANCY AND IS MAXIMAL DURING LACTATION.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BIN/MOGGINEPARTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U67065; AAB51034.1; -. EMBL; S80642; AAB35893.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
                           189
                                                                                   129
                                                                                                               104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
SCCIQ 222
                           MCLIK 193
                                                                                                          LDGRATLLIRDVRVSDQGEYRC--LFKDNDDFEE----AAVYLKVAAVGSDPQIS-MTVQE
                                                                                                                                                                    AELTCGFSPNASSEYM---ELLWFRQTRSTAVLLYRDGQEQEGQQMTEYRGRATLATAGL 103
                                                                                                                                                                                              ATLSCGH--NVSVEELAQTRIYWQKEKKMVLTMMSGD-----MNIWPEYKNR----TIFD 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:103118; Btn1a1.
                                                      NGEMELECTSSGWYPEPQVQWRTGNREMLPSTSESKKHNEEGLFTVAVSMMIRDSSIKNM
                                                                               SNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSF
                                                                                                                                     ITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPT 128
                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR003006; Ig_MHC.
IPR003596; Ig_v.
IPR003877; SPRY.
IPR003878; SPRY_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001870;
                                                                                                                                                                                                                                                                                               524
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117
191
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423
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                                                                                                                                                                                                                                     10.4%; Score 119; DB 1; Length 524; 23.8%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gamma_carbxylse.
                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                                                           34;
                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
D -> DD (IN REF. 2).
V -> F (IN REF. 2).
E -> D (IN REF. 2).
R -> S (IN REF. 2).
V -> E (IN REF. 2).
T -> K (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                     SL -> FF (IN REF. 2).
PRRV -> LAEY (IN REF.
                                                                                                                                                                                                                                                                                                                       DIPLSPLGEGCTSGDKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin domain; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BUTYROPHILIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                             333F4DE2C7704480 CRC64;
                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                          87;
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                                                                                                                                                                                                                          Indels
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GHSLVPAGGRLYFWRQRH
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XYENLA STANDARD; PRT; 1088 AA.
P16170;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Neural cell adhesion molecule 1, large isoform precursor (N-CAM 180)
                                                                                                                                                                                                                                            SMART; SM00060; FN3; 2.
SMART; SM00408; IGC2; 5.
                                                                                                                                                                                                                                                                         Pfam; PF00041; fn3; 2
Pfam; PF00047; ig; 5.
                                                                                                                                                                                                                                                                                                                                                     EMBL; M25696; AAA49909.1; -. PIR; S09600; IJXLNL. HSSP; P56276; 1TLK.
                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no rest
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modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 17:10321-10335(1989).
-!- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF NEURITES, ETC.
                                                                                                                 DOMAIN
                                                                                                                                TRANSMEM
                                                                                                                                                 DOMAIN
                                                                                                                                                                                CHAIN
                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                          Cell adhesion; Glycoprotein; Transmembrane; Repeat; Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS
- N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.
-i- TISSUE SPECIFICITY: EXPRESSED IN NEURON AND IN PRESUMPTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=90098871; PubMed=2481269;

Krieg P.A., Sakaguchi D.S., Kintner C.R.;

"Primary structure and developmental expression of a large
                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecule (NCAM).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytoplasmic domain form of Xenopus laevis neural cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8355;
                                                                                                                                                                                                            [mmunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kenopodinae; Kenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE: THE MRNA ENCODING THIS LD-NCAM IS THE MAJOR TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLY NEURAL DEVELOPMENT
                                                                                                                                                                                                                                                                                                    IPR003961; FN_III.
IPR003006; Ig_MHC.
IPR003598; Ig_c2.
                                                                                                                                                                               20
    705
723
1088
100
193
289
386
480
589
                                                                                                                                                                               1088
                                                                                                                                                                                                            Alternative splicing;
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
IG-LIKE C2-TYPE DOMAIN 4.
IG-LIKE C2-TYPE DOMAIN 5.
PIBRONECTIN TYPE-III 2.
                                                                                                                                                                             NEURAL CELL ADHESION MOLECULE 1,
                                                                                                                                                                                                            Signal.
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Search completed: June 18, 2002, 11:47:43 Job time: 226 sec
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                                                                                                                                                                                                                                                                                                                       DOMAIN
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DISULFID
DISULFID
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DISULFID
DISULFID
CARBOHYD
                                                                                                                                 174
                                                                                                                                                                                       134 -IICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN-----MTTNH 186
                                                                                                                                                                                                                     18
                                                                                                                                                           78
                                                                                                                                               LALRÉSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEI----PTSNIRR- 133
                                                                                                                                                                                                      EVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRTIFDITNNLSIVI 77
                                                                      VVLSCDADGFPDPEISWLKKGEPI-----EDGE-----EKISFNEDQSEMTIHH 271
                                                                                                                                 RGIKKTDEGTYRC-----EGRILARGEINYKDIQVIVNVP-PTIQARQLRVNATANMAES 227
                                                                                                                                                                                                                                                                                                                         149
158
41
136
232
323
420
82
219
310
310
341
417
443
4472
804
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162
193
186
282
282
379
473
82
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443
472
473
1049
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                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL).

MISSING (IN ISOFORM N-CAM 140).

8 MW; 62738B55B03F3E83 CRC64;
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HEPARIN-BINDING (POTENTIAL).
PROBABLE.
PROBABLE.
PROBABLE.
PROBABLE.
PROBABLE.
PROBABLE.
PROBABLE.
PROBABLE.
                                                                                                                                                                                                                                                                                                                         MW;
                                                                                                                                                                                                                                                 Indels 47;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
SPTREMBL_19:*

1: sp_archea:*
2: sp_bacteria
3: sp_fung1:*
4: sp_human:*
5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
8: sp_organe1:
9: sp_organe1:
9: sp_plane:*
11: sp_plane:*
11: sp_rodent:
12: sp_virus:*
13: sp_virus:*
14: sp_unclass
15: sp_bacteri
17: sp_archea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         June 18, 2002, 11:43:32; Search time 26.58 Seconds (without alignments)
1405.828 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-454-651B-23
1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                   sp_archea:*
sp_bacteria:*
sp_fungi:*
                                                                                                               sp_organelle:*
sp_phage:*
sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLSHFCSGVIHVTKEVKEVA.....LRVNQTFNWNTTKQEHFPDN 216
               sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
                                                                                                                                                                  sp_invertebrate:*
sp_mammal:*
sp_mhc:*
   sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                          562222
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

09tqs8 (0 Q9nOtO (37 035187	61.4 235 6 Q9TQS8 Q9tqs8 61.4 235 6 Q9NOTO Q9nOtO	61.4 235 6 Q9TQS8 Q9tqs8		62.4 296 6 046405 046405	62.6 304 6 Q9TQX1 Q9tqx1	64.7 292 6 002758 002758	64.7 292 6 Q9GMZ8 Q9gmz8	66.2 229 6 Q9TT71 Q9tt71	66.4 297 6 Q9BE99 Q9be99	66.4 288 6 Q9TT70 Q9tt70	66.5 230 6 Q9N2I3 Q9n2i3	94.4 289 6 Q28347 Q28347	94.4 288 6 Q9BDN6 Q9bdn6	95.7 288 6 Q28499	97.3 288 6 077684 077684	Score Match Length DB ID	Requilt Ouerv
_	035187 rattus norv	Q9n0t0 canis famil	Q9tqs8 canis famil	046405 bos taurus	_			-		Q9tt70 sus scrofa	Q9n2i3 sus scrofa	Q28347 cercocebus	Q9bdn6 cercocebus	Q28499 macaca mula	077684 macaca neme	Description	

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ALIGNMENTS

	KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSI 147	88 KI	DЬ
	KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121	62 KI	Qy
	LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 87	28 L	Db
	LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 61	2 L:	Qy
0	97.3%; Score 1118; DB 6; Length 288; Similarity 97.7%; Pred. No. 4.6e-96; 0; Conservative 1; Mismatches 4; Indels 0; Gaps	Query Match Best Local Matches 21	X #10
	INCE 288 AA; 33131 MW; /6BBC42839E9AB/9 CKC64;	SEQUENCE	QS
	SM00410; IG_like; 1.	SMART;	DR
	Ptam; PFUUU47; 1g; 1. SMART: SMO0409: IG: 1.	Ptam; I	DR DR
	Pro; IPR003006; Ig_MHC.	InterPro;	DR
		InterPro;	DR
	Pro; IPR003599; Iq.	InterPro;	DR
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	Kraus G., Hnatyszyn J.H.; Araus G., Hnatyszyn J.H.;	Kraus (Z Z
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	aca.	Cercopi	8
	Primates; Catarrhini; Cercopithe	Mamma 1 i	88
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Q28499;
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SMART; SM00409; IG; 1.
SMART; SM00410; IG_like; 1.
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EMBL; U19840; AAA86706.1; -.

EMBL; AF344849; AAK37609.1; -.
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                                                                                                                                                                                                                                SEQUENCE
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             MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                            MTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFPDN
                                                    KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSI 147
                                                                                              KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
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IPR003600; Ig_like.
IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                 F., Bostik P., Mayne A.E., King C.L.,
., Ansari A.A.;
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
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                                                                                                                                                                          Conservative
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33141 MW;
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96.3%;
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Pred. No. 2.2e-94;
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242
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Q28347;
Q28347;
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01-NOV-1996 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
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Q9BDN6;
Q1-JUN-2001
01-JUN-2001
01-DEC-2001
MEDLINE=96003435; PubMed=7561102;
Villinger F., Brar S.S., Mayne A., Chikkala N., A
"Comparative sequence analysis of cytokine genes
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                            TISSUE=BLOOD;
                                                                                Cercopithecinae; Cercocebus.
NCBI_TaxID=9530;
                                                                                                                                       Cercocebus
                                                       SEQUENCE FROM N.A.
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SMART; SM00409; IG; 1.
SMART; SM00410; IG_like; 1.
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InterPro; IPR003600; Ig_like
InterPro; IPR003006; Ig_MHC.
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Immunogenetics 53:315-328(2001).
EMBL; AF344839; AAK37535.1; -
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                                                                                                                        s (red-crowned mangabey).
Chordata; Craniata; Vert
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J. Immunol. 155:3946-3954(1995).
EMBL; U19833; AAA86700.1; -.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 1.
SMARF; SM00410; IG_like; 2.
NON_TER 289 289
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                     InterPro; IPR003599; Ig. InterPro; IPR003500; Ig_like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003006; Ig_MHC. Pfam; PF00047; Ig; 2. SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                   STRAIN-LANDRACE; TISSUE-SPLEEN;
Wada M., Amae S., Hoshi M., Nio M., Ohi R.;
"Porcine CD80(B-7) mRNA, partial cds.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AB026121; BAA90700.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                            CD80 PROTEIN PRECURSOR.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                          SEQUENCE
                                                                                                                                                                 SIGNAL
                                                                                                                                                                              Signal.
                                                                                                                                                                                          SMART; SM00409; IG; 1.
SMART; SM00410; IG_like; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LSHFCSGVIHYTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY
                                                                                                                                                                                                                                                                                                                                                                                                 scrota (Pig).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTTNHSFVCLIKYGHLRVNQTFNWNTPKQEHFPDN 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYCQKEKKMVLTMISGDMNIWPEY
                                                                             140;
 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS
                         GLFDFCSGIVQVTKTVKEIAVLSCDYNISTEELTRVRIYWQKDNEMVLAVMSGKVKVWPK
                                                   GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE
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30
230 AA;
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                                                                            Conservative
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                                                                                                                                         29 P
230 P
26028 MW;
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95.38;
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                                                                                    66.5%;
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                                                                                      Score 764; DB 6
Pred. No. 3e-63;
                                                                                                                                          POTENTIAL.
EB63AD172663C4A4 CRC64;
                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5ED6A3F6A3C59297 CRC64;
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                                                                                                    6;
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                                                                                                   Length 230;
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PAC II

Q9BE99; 01-JUN-2001

(TrEMBLrel.

17,

Created)

Q9BE99

PRELIMINARY;

PRT;

297 AA

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RESULT Q917770
ID TT770
Q9 DT Q9 DT Q9 DT Q9 DT Q1 DT 
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RESULT
Q9BE99
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01-MAY-2000
01-MAY-2000
01-DEC-2001
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Faas S.J., Giannoni M.A., Mickle A., Kiesecker C.L., Reed D.J., Fodor W.L., Mueller J.P., Matis L.A., Rother R.P.; "Primary Structure and Functional Characterization of a Soluble, Alternatively Spliced Form of B7-1."; J. Immunol. 164:6340-6348(2000).
EMBL; AF203443; AAF22750.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9TT70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00410; IG; 1.
SMART; SM00410; IG_like;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. 
MEDLINE=20302785; PubMed=10843688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTK 209
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                                                                                                                                 NMTTNHSFMCLIKYGHLRVNQTFNW-NTTKQE 211
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                                                                                                         NVTGNHSFMCLVKYGGLTVSQTFNWQKSAKRE 233
                                                                                                                                                                                                                                      ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
                                                                                                                                                                                                                                                                                                                 YENRTFTDYTNNLCIVILALRLSDNGTYTCVVQKRERGSYKLEHLTSVKLMVKADFPVPS
                                                                                                                                                                                                                                                                                                                                                                                                                     GLFDFCSGIVQVTKTVKEIAVLSCDYNISTEELTRVRIYWQKDNEMVLAVMSGKVKVWPK 81
                                                                                                                                                                                                          ITALGNPSPNIKRIRCSTSGGFPEPHLSWLENGEELNATNTMLSQDPETELYMISSELDF
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288
288
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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>288
288
32510 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 288;
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Sus.
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Best Local S
Matches 141
                                                                                                                                                                                                                                            Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Crania:
Mammalia; Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                              O9TT71;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
                                                                                     Faas S.J., Giannoni M.A., Mickle A., Kiesecker C.L., Reed D.J., Fodor W.L., Meuller J.P., Matis L.A., Rother R.P., "Primary Structure and Functional Characterization of a Soluble, Alternatively Spliced Form of B7-1.";
                                                                                                                                                                                                                                                                                                                          CD80 OR CD80/B7-1.
  TISSUE-SPLEEN;
                                                                 Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9TT71
                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
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SMART; SM00409; IG; 1.
SMART; SM00410; IG_like; 1.
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InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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isoforms.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001
01-DEC-2001
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Hayashi Y.,
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                                                                                                                                                                                                                                                                                                                                                  PROTEIN PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NYTGNHSFMCLVKYGGLTVSQTFNWQKSAKRE
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Y., Ohi R.;
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297 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AΑ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 P
297 C
33438 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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Pred. No. 5.
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; 23109711EA63EF23 CRC64;
                                                                                                                                                                                                                                                   Craniata; Vertebrata; actyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i.8e-63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                      Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297;
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Best Local
        InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 11.
SEQUENCE 292 AA; 33540 MW;
                                                                                                                                                                                                                                                                                                                  Q9GMZ8
Q9GMZ8;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                             Nishimura Y., Shinojima M., Miyazawa T., Sato E., Nakamura K., Izumiya Y., Ikeda Y., Mikami T., Takahashi E.; "Molecular cloning of the cDNA encoding the feline B-lymphocyte activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which interact with human CTLA4-1g."; Eur. J. Immunogenet. 27:427-430(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal.
                                                                                                                                                                                                                                                Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2000) to the EMBL/GenBank/DDBJ EMBL; AF203442; AAF22749.1; -. EMBL; AB038153; BAA90764.1; -. InterPro; IPR003599; Ig. InterPro; IPR003600; Ig_like. InterPro; IPR003060; Ig_MHC.
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          B-LYMPHOCYTE ACTIVATION
                                                                                                                                                                                                MEDLINE=20485322; PubMed=11029611;
                                                                                                                                                                                                                                         NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 1.
SMART; SM00410; IG_like;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wada M., Amae S., Hoshi M., Nio M., Ishii T., Ohi R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE
                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NMTTNHSFMCLIKYGHLRVNQTFNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLFDFCSGIVQVTKTVKEIAVLSCDYNISTEELTRVRIYWQKDNEMVLAVMSGKVKVWPK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                           NVTGNHSFMCLVKYGGLTVSQTFNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITALGNPSPNIKRIRCSTSGGFPEPHLSWLENGEELNATNTMLSQDPETELYMISSELDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YENRTFTDVTNNLCIVILALRLSDNGTYTCVVQKRERGSYKLEHLTSVKLMVKADFPVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isoform of Porcine CD80.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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67.8%;
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0 MW;
                                                                                                                                                                                                                                                                                                      16, Last sequence update)
19, Last annotation update)
ANTIGEN B7-1 (CD80).
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                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 761; DB 6;
Pred. No. 5.7e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD80 PROTEIN.
; C3AD172663C4A4ED CRC64;
           ED9AEECE10D30401 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205
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                                                                                                                                                                                                                                                                                                                                                                           292 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 229;
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                                                                                                                                                                                                                                                    Euteleostomi;
Felis.
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0

Best Local Similarity

64.7%; 63.3%;

Score 743; Pred. No.

3.7e-61;

Length 292;

Query Match

В7

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OCC MAD RESULT ON OCC PT OCC MAD OCC PT OCC MAD OCC MA
    Q9TQX1
ID Q
AC Q
DT 0
DT 0
DT 0
DT 0
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Best Loc
Matches
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  Q9TQX1;
Q9TQX1;
01-MAY-2000
01-MAY-2000
01-DEC-2001
B7-1 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
T-CELL SPECIFIC SURFACE GLYCOPROTEIN B7-1.
Felis silvestris catus (Cat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Felis catus t-cell specific surface glycoprotein Thesis (1996), Veterinary Pathobiology, Texas Asm EMBL; U5775; AASS3575.1; ... Interpro; IPR003600; Ig_like. Interpro; IPR003006; Ig_MHC. Pfam; PF00047; 1g; 1. SMART; SM00410; IG_like; 2. SEQUENCE 292 AA; 33482 MW; 6F117E7852B7950F CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; NCBI_TaxID-9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hash S.M., Collisson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         148
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                                                                                                                                                                                                                                                                                                                                                                SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI
                                                                                                                                                                                                                                             MTNNHSFLCLVKYGNLLVSQIFNWQ--KSEPQPSN
                                                                                                                                                                                                                                                                                                                                         TDLGNPSHNIKRIMCLTSGGFPKPHLSWLENEEELNAINTTVSQDPETELYTISSELDFN
                                                                                                                                                                                                                                                                                                                                                                                                                                   KNRTFTDVTDNHSIVIMALRLSDNGKYTCIIQKIEKGSYKVKHLTSVMLLVRADFPVPSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFYFCSGIIQVNKTVEEVAVLSCDYNISTKELTEIRIYWQKDDEMVLAVMSGKVQVWPKY
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       PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136;
    (TrEMBLrel. )
(TrEMBLrel. )
(TrEMBLrel. )
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                                                                                                                          PRELIMINARY;
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13,
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33;
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                        Last sequence update)
Last annotation update)
                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 743; DB 6;
Pred. No. 3.7e-61;
3; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6F117E7852B7950F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
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Best Local Similarity
Matches 130; Conserv
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EMBL; AF106824; AAF17295.1; -.
EMBL; AF106829; AAF17293.1; -.
EMBL; AF106829; AAF17293.1; JOINED.
EMBL; AF106830; AAF17293.1; JOINED.
EMBL; AF106831; AAF17293.1; JOINED.
EMBL; AF106832; AAF17293.1; JOINED.
                                                                                                                                                                                                                              O46405 PRELIMINARY; PRT; 296 AA.
O46405;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CD80 ANITGEN PRECURSOR (FRAGMENT).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Boyinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                          Parsons K.R., Howard C.;
"Clonling of cattle CD80.";
Immunogenetics 49:231-234(1999).
EMBL; Y09950; CAA71081.1;
                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=99115507; PubMed=9914337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 1. SMART; SM00409; IG; 1.
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InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canis familiaris (Dog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-9615;
                        InterPro;
                                                                                                                                                                                                                 NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFYFCSGIIQVNKTVKEVAVLSCDYNISTTELMKVRIYWQKDDEVVLAVTSGQTKVWSKY 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITSNHSFYCLVKYGDLTVSQIFNWQKSVEPHPPNN
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    IPR003599;
IPR003600;
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304 B'
34454 MW;
īg_like.
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B7-1 PROTEIN
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Best Local
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Best Local (
                                   Matches
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EMBL; AF106825; AAF17296.1; -.
EMBL; AF106825; AAF17294.1; -.
EMBL; AF106829; AAF17294.1; JOINED.
EMBL; AF106829; AAF17294.1; JOINED.
InterPro; IPR003599; Ig.
InterPro; IPR003500; Ig_11ke.
InterPro; IPR003600; Ig_1MRC.
InterPro; IPR003600; Ig_MHC.
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Pfam; PF00047; Ig; 2.
SMART; SM00409; IG; 1.
SMART; SM00410; IG_like; 1.
Signal.
SIGNAL 1 25
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Q9TQS8;
01-MAY-2000
01-MAY-2000
01-DEC-2001
                                                                                            CHAIN
SEQUENCE
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SEQUENCE
                                                                                                                 Signal.
                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00410; IG_like; 1.
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                             SECRETED B7-1 PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                  Yang S., Sim G.-K.;
"New Forms of Dog CD80 and CD86 Transcripts that Encode
                                                                                                                                                                                                                                                                                                                                                                  Canis familiaris (Dog).
                                                                                                                                                                                                                                                               Molecules."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 LDFNMTTNHSFMCLIKYGHLRVNQTFNWNTTK 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118
                                 Local Similarity 61.5 hes 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
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1 GLSHFCSGVI--HVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIW 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPSISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSK 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEYKNRTIFDIINNLSIVILALRPSDEGTYECVVLKYE-KDAFKREHLAEVTLSVKADFP 117
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235 AA;
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296 AA;
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
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                                                                                         33 F
235 S
26917 MW;
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296
33618 MW;
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63.2%; Pred. No. 9e-
tive 28; Mismatches
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                                            61.4%; Score 705; DB 6; 61.5%; Pred. No. 9.7e-58;
                                  33;
                                                                                         POTENTIAL.
SECRETED B7-1 PROTEIN.
; CC08CAA676BCB40A CRC64;
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                                  Mismatches
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                                  47;
                                                      Length 235;
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                                  Indels
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Best Local S
Matches 128
O35187;
O35187;
01-JAN-1998
01-JAN-1998
01-DEC-2001
B7.1.
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01-OCT-2000 (TremBirel. 15, Last sequence up
01-DEC-2001 (TremBirel. 19, Last annotation
T-CELL CO-STIMULATORY PROTEIN B7-1.
B7-1.
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Q9NOTO;
01-OCT-2000
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EMBL; AF257653; AAF69006.1;
InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
Pfam; PR00047; Ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00410; IG; 11.
SMART; SM00410; IG, 11ke; 1.
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Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Craniata; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENRTFADFTNNLSIVIMALRLSDNGKYTCIVQKTEKRSYKVKHMTSVMLLVRADFPVPSI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
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                      (TrEMBLrel. 05, Created)
(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
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                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.4%; Score 705; DB 6; L
61.5%; Pred. No. 9.7e-58;
73. Mismatches 47;
                                                                                                                                         PRT;
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Search completed: June 18, Job time: 232 sec
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OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

STRAIN=FISCHER;

RX MEDLINE=99176848; PubMed=10078962;

RX MEDLINE=99176849; PubMed=10078962;

RX MEDLINE=99176849;

RX MEDLINE=9176849;

RX MEDLINE=99176849;

RX MED
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                                                                                                                                                                                               180 FNMTTNHSFMCLIKYGHLRVNQTFNW 205
                                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                            151 NITESGNPSADIKRITCFASGGFPKPRLSWLENGRELNGINTTISQDPESELYTISSQLD 210
                                                                                                                                                                                                                                                                                                                                                                                                                                    91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLSHFCSGVI-HVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWP 59
                                                                                                                                                                                                                                                                                                                                   SISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 179
                                                                                                                                                                                                                                                                                                                                                                                                                         EYKNRTVYDIANNYSFSLLGLILSDRGTYTCVVQRYEGESYVVKHLTTVELSVRADFPTP 150
                                                                                                                                                               FNTTYDHFIDCFIEYGDAHVSQNFTW 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTP 119
                           2002, 11:47:24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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1: /SIDS1/gcgdata/
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1149
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/SIDS1/gcgdata/hold-genesed/geneseqp-emb1/AA1989.DAT: *
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/gcgdata/hold-geneseq/geneseqp-embl/AA2001
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and	score greater than or equal to the score of the result being printed,	Pred
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SUMMARIES

Result No.	Score	% Query Match L	Length DB	DB	ID	Description
ъ	1149	100.0	288	16	AAR67989	Human B lymphocyte
2	1149	100.0	288	18	AAW38414	B7-1. Homo sapien
ω	1149	100.0	288	20	AAW67804	Human B7 protein s
4	1149	100.0	288	20	AAW73640	Human B7-2 antigen
ъ	1149	100.0	288	21	AAB37087	Human B lymphocyte
6	1149	100.0	288	21	AAY99966	Human B7 protein.
7	1149	100.0	288	21	AAY44289	Human B7.1 co-stim
8	1149	100.0	288	21	AAY54920	Human B7.1 protein
9	1149	100.0	288	22	AAU05121	Colorectal tumour
10	1149	100.0	288	22	AAB19959	Human B lymphocyte
11	1149	100.0	473	18	AAW41415	Human B7.1-murine

45	44	43	42	41	40	ω.	38	37	36	35	34	ω	32	3	30	29	28	27	26	25	24	23	22	21	20	19	8	17	9	5	4	ω	12
182	182	182	188.5	200.5	200.5	200.5	250.5	250.5	305	311	349.5	558	558	558	558	561	561	561	561	705	719	739	739	743	743	761	1047	1138	1143	1143	1143	1144	1146
5	15.8	5	σ,	17.4	17.4	7.	1	21.8	σ,	7.		ω.		.00		œ	œ	48.8			62.6		*		-	٠,	-	۳.			۳.	99.6	
246	246	244	280	332	329	329	226	212	200	214	173	306	306	306	306	320	306	306	306	235	304	292	292	292	292	229	208	480	492	488	488	475	251
22	20	20	20	20	21	21	16	16	16	16	20	21	21	20	20	16	22	16	16	20	20	21	21	21	21	22	18	20	19	22	20	18	20
AAB83837	AAW86005	AAW90209	AAY41078	AAY41079	AAY32278	AAY32285	AAR82903	AAR82902	AAR82900	AAR82901	AAY41082	AAY99967	AAB37088	AAW73641	AAW67805	AAR82892	AAB19960	AAR67990	AAR82893	AAY41077	AAY41075	AAY32277	AAY32284	AAY32276	AAY32283	AAY97780	AAW35858	AAW90206	AAW42338	AAB83836	AAW86004	AAW38415	AAW90208
Amino acid sequenc		hB7.1his soluble f	ine B7-2S prot	в7-2 р	86 (B7-2) L	ine CD8	B7 - 1	Mouse B7-1 IgV-lik	4	Η.	7-	e B7 pro	B ly	в7 -	B7 pr		\vdash	Murine B lymphocyt	B7 -	7-1	_	80 (B7	D80	0 (B7	CD80	uble porc	Human B7.1 for use	sol	-Ig-al	Amino acid sequenc	Human B7-1.5T4.1 p	Soluble B7-1-Ig.	ս-ց1

ALIGNMENTS

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RESULT
AAR67989
/label= intracellular Misc-difference 53..55
                                                                                                                                                                                                           B lymphocyte antigen; B7-1; B cell activation antigen; CD28; ligand; T cell surface antigen; transmembrane protein.
                                                                                                                                                                                                                                                                                                 AAR67989 standard; Protein; 288
                                                                                                                                                                         Key
                                                                                                                                                                                                                                       Human B lymphocyte antigen B7-1 (hB7-1).
                                                                                                                                                                                                                                                          21-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                               AAR67989;
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                 /label= see above Misc-difference 186..188
                                    Misc-difference 98..100
                                                     /label= N-linked glycosylation Misc-difference 89..91
                                                                                             Domain
                                                                                                               Domain
                                                                                                                                 Domain
                                                                                                                                                               Protein
                                                                                                                                                                                          Homo sapiens.
                                                                                                                                /label= signal sequence
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35..242
                                                                                                               /label= extracellular 243..269
                                                                                             /label= transmembrane 270..288
                                                                                                                                                                       Location/Qualifiers
                                              /label≖ see above
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RESULT
AAW38414
ID AAW3
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AC AAW3
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                                                                                                                                                                                                                                                                            Matches 216;
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-1993;
19-AUG-1993;
03-NOV-1993;
            AAW38414;
                                                                                                                                                                                                                                                                                                                                                    Q81371 is in pCDM8 vector. It is derived from lymphoid B cells, cell line Raji, clone no. 13. Its position in the genome is chromosome/segment 3. It was published by Freeman, F.J. et al., J. of Immunology, 143: 8: 2714-2722, 15th October 1989. It can be found in Genbank at Accession no. M27533. The encoded protein, R67989, binds both human CTLA4 and human CD28. It is related to human hB7-2 (see Q81351) and murine hB7 (see Q81372).
                                AAW38414 standard;
                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Freeman
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; pages 111-113; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful for enhancing or suppressing T-cell mediated immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9503408-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-1994;
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                                                                                          207
                                                                                                                181
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                                                       N
                                                                                    ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
                                                                                                                                                                                          YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                                      GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                              yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps\\
                                                                                                                                                                                                                            glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1995-075236/10.
DB; AAQ81371.
                                                                                                                                  isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavsskldf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DANA FARBER CANCER INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPLIGEN CORP
                                                                                                                                                                                                                                                                                                                                    288 AA;
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gray GS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-0101624.
93US-0109393.
93US-0147773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94WO-US08423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= see above 35..138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= see above 232..234
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139..236
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                                Protein;
                                                                                                                                                                                                                                                                        100.0%; Score 1149; DB 16; 100.0%; Pred. No. 2.6e-103; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Greenfield
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nadler
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                               Length 288;
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                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                            Query Match
       Homo sapiens
                                                  Human B7 protein sequence
                     Human; B7; transfection; mammal; tumour cell; sarcoma; co-stimulation; T- cell; CD28; CTLA4; ligand; T-lymphocyte response; metastasis.
                                                                        13-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                           New xanthene derivatives useful as immunomodulators - e.g. methyl 2-(carboxymethylsulphinyl)-5,7-dichloro-3,8-dihydroxy-6-methyl-9-oxo-9H-xanthene-1-carboxylate.
                                                                                                          AAW67804 standard;
                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                 The present sequence was used in the development of a novel for screening for compounds that inhibit or enhance binding
                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 4; 117pp; English.
                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                          to B7-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT96358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-450803/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hattori M, Hida T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-1996;
05-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP795554-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening; inhibitor; enhancer; binding; CD28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-APR-1998 (first entry)
                                                                                                                                                           207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-SEP-1997.
                                                                                                                                                                                                                                                                                                          Local Similarity
hes 216; Conserv
                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                       27
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                                                                                                                                                               NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                         YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                        nmttnhsfmclikyghlrvnqtfnwnttkqehfpdn 242
                                                                                                                                                                                                                                                                                                                                                         288 AA;
                                                                                                                                                                                                                                                                                                            Conservative
                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96JP-0262085
96JP-0047795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97EP-0301438
                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kurokawa T,
                                                                                                            288
                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                 Score 1149; DB 18;
Pred. No. 2.6e-103;
                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakanishi A;
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                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                           288;
                                                                                                                                                                                                                                                                                                                                                                                 l method
J of CD28
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Query Match
Best Local S
Matches 216
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Peptide
                                                                                  The modified tumour cells can be used for inducing an anti-tumour T-lymphocyte response in a subject and are effective against both modified and unmodified tumour cells. The modified tumour cells can also be administered to prevent or inhibit metastatic spread of a tumour or to prevent or inhibit recurrence of a tumour following therapeutic
                                                                                                                                                                                                              which allows the induction of an anti-tumour response by T cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                        This sequence represents the amino acid sequence of a human B7 protein. The coding sequence can be used to transfect mammalian tumour (sarcoma) cell so that the B7 protein is expressed by the tumour cell and has the ability to co-stimulate T cells and bind CD28 or CTLA4 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                              Disclosure; Column 31-34; 24pp; English
                                                                                                                                                                                                                                                                                                                                                              03-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                      Sequence
                                                                                                                                                                                                                                                              N-PSDB; AAX00757.
                                                                                                                                                                                                                                                                                                                                                                                                       12-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                            US5858776-A
 Local Similarity hes 216; Conserv
                                                                                                                                                                                                                                                                        1999-119893/10.
                                                                                                                                                                                                                                                                                                                             DANA FARBER CANCER INST INC HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                             Freeman GJ,
                                                      288 AA;
 Conservative
                                                                                                                                                                                                                                                                                                                                                             93US-0147772.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= ".
211..213
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207..2
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89..91
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53..55
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35..288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98..100
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Ig V-set domain"
140..236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Asn is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 228
 100.0%; Score 1149; DB 20; 100.0%; Pred. No. 2.6e-103; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Asn is N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Asn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "intracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "extracellular domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                "Ig C-set domain"
                                                                                                                                                                                                                                                                                              Glimcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is
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                                                                                                                                                                                                                                                                                              LH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein"
                                                                                                                                                                                                                                                                                              Nadler LM,
                                                                                                                                                                                                                                                                                              Ostrand-Rosenberg
  Indels
                     Length
                      288;
  0;
  Gaps
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1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKWVLTMMSGDMNIWPE

glshfcsgvihvtkevkevatlscghnvsveelagtriywqkekkmvltmmsgdmniwpe

YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120

19 27

Query Match
Best Local Similarity Matches 216;

Conservative

0

Mismatches

Indels

0;

Gaps

0;

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RESULT
AAW73640
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                                                         This sequence is the human B7-2 antigen, which can be used in the method of the invention. The method is for transfecting an isolated mammalian tumour cell with an exogenous nucleic acid molecule encoding a mammalian B7-2 molecule, where the B7-2 molecule is expressed in the tumour cell is capable of costimulating a T cell and is capable of binding a CD28 or CTLA4 ligand. The method is useful for treating tumours
                                                                                                                                                                                                                      Tumour cell transfected to express B7-2 molecule therapy by stimulating T-cell response
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5861310-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B7-2 antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human B7-2 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW73640 standard; Protein; 288
                                                                                                                                                                                             Disclosure; Column 37-40; 27pp; English
                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                              WPI; 1999-130394/11
                                                                                                                                                                                                                                                                                                        Freeman GJ,
                                                                                                                                                                                                                                                                                                                                                             30-MAY-1995;
03-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                        Sequence
                                                                                                                                                                                                                                                                                                                                   (DAND ) DANA FARBER CANCER INST INC
                                                                                by stimulating a T-cell response against tumour cells in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YKNRTIFDITUNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYMQKEKKMVLTMMSGDMNIMPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nmttnhsfmclikyghlrvnqtfnwnttkqehfpdn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NMTTNHSFMCLIKYGHLRVNOTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavsskldf 206
                                                                                                                                                                                                                                                                 AAV55786
                                                         288
                                                                                                                                                                                                                                                                                                        Gray GS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mammalian tumour cell; T cell costimulation; CD28 ligand;
                                                                                                                                                                                                                                                                                                                                                             95US-0456104.
93US-0147773.
                                                                                                                                                                                                                                                                                                                                                                                                       95US-0456104
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T-cell response;
                                                                                                                                                                                                                                                                                                         Nadler LM;
  Score 1149; DB 20;
Pred. No. 2.6e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
              Length 288;
                                                                                                                                                                                                                                         useful for tumour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
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RESULT AAB37087
ID AAB37087
ID AAB37087
ID AAB3
XX AAB3
XX AAB3
XX Immu
XX Immu
KW Immu
KW Immu
KW T Ce
XX US61
XX US61
XX IO-0
PR 26-J
PR 26-J
PR 26-J
PR 03-W
XX (PAN
PR 03-W
XX (PAN
PR N-PS
XX (PAN
PR N-P
The invention relates to an isolated nucleic acid molecule encoding a fusion protein comprising a first nucleotide sequence encoding a first competitive, and a second nucleotide sequence encoding a second peptide. The first nucleotide sequence hybridizes in 6 x sodium chloride/sodium controlled sequence hybridizes in 6 x sodium chloride/sodium controlled sequence hybridizes in 6 x sodium chloride/sodium controlled for controlled sequence which encodes a human or murine controlled for the ability to bind CD28 or CTLA4. The first peptide has an amino acid controlled that is identical or at least 50% identical with the controlled is sequence that is identical or at least 50% identical with the controlled is septide is septially an immunoglobulin constant region. This sequence controlled is esquence in the human B7-2 peptide (AAB37085). The second comparison with the B7-2 sequence. The human B7-2 protein is an example of a first peptide sequence of the invention. The nucleic acid molecules are useful in various expression vectors to direct synthesis of the corresponding proteins or peptides in a variety of hosts, particularly calds are also useful for enhancing the immunogenicity of a mammalian cell, e.g. tumour cell (sarcoma) or an antigen presenting cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids and fusion proteins of CTLA4/CD28 ligands, useful for enhancing or suppressing T cell-mediated immune responses, especially during tissue, skin or organ transplantation, or in graft-versus-host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-1993;
19-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunomodulator; fusion protein; human; murine; mouse; lymphocyte; CD28; antigen; extracellular domain; CTLA4; immunoglobulin constant region; immunogenicity; tumour; sarcoma; antigen presenting cell; macrophage; T cell-mediated immune response; transplantation; vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Column 87-90; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-NOV-1993;
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DB; AAC84051.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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93US-0109393.
93US-01477773.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (macrophage). The fusion proteins or peptides are useful for enhancing or suppressing T cell-mediated immune responses, e.g. in situations of tissue, skin or organ transplantation, or in graft-versus-host disease. The proteins are also useful for enhancing the efficacy of vaccination against a variety of pathogens, and may also be used to upregulate an immune response against a particular pathogen during an infection or against a tumour in a tumour-bearing host.
                                    Modified-site
                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                          Human B7 protein
                                                                                                                                                                                                                                                                                                                                                                                                                  10-JAN-2001
                                                           Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nmttnhsfmclikyghlrvnqtfnwnttkqehfpdn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps 146
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216; Conserv
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                                                                                  /note=
207..2
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211..2
                                                                                                                                                                                                                                 /label=
35..138
                                                                                                                                                          98..100
                                                                                                                                                                                  89..91
                                                                                                                                                                                                                                                        /label= signal_peptide 35..242
                                                                                                          186..188
                                                                                                                                  /note= "N-linked glycosylation site"
139..236
                                                                                                                                                                                           /note= "N-linked glycosylation site"
                                                                                                                                                                                                                                                                                            Location/Qualifiers
                        note= "N-linked"
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Pred. No. 2.6e-103;
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Best Local S
Matches 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein. The cDNA encoding this sequence was isolated from a Burkitt lymphoma cell line cDNA library. Selection of cDNA clones was based on expression of B7, as detected by the anti-B7 monoclonal antibody. The human B7 cDNA was used in hybridisation analysis to isolate the murine B7 cDNA (see AAA61329). The B7 nucleic acid sequences may be used to generate transgenic, knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The expressed B7 protein is useful for enhancing or blocking activated T cell mediated immune responses and immune function. Modification of B7 expression is useful in the treatment of autoimmune diseases (e.g. rheumatoid arthritis or multiple sclerosis), herpes simplex, influenza, the common cold and HIV. It is also useful in tissue and organ transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
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01-OCT-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 4; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regulating T cell mediated immune responses or viral diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nadler LM, Freeman GJ, Freedman AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides encoding a B7 activation antigen, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                AAY44289;
                  29-FEB-2000
                                                                              AAY44289 standard; Protein;
                                                                                                                                                                                                                         147
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                                                                                                                                                                                         181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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                                                                                                            7
                                                                                                                                                                                                                                                                                 yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps 146
                                                                                                                                                                                                                                                                                                    YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                                                                                                                                             glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe 86
                                                                                                                                                                                                                                                   ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
                                                                                                                                                                                                                    isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavsskidf 206
                                                                                                                                                       ### nmttnhsfmclikyghlrvnqtfnwnttkqehfpdn 242
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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ilarity 100.0%;
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90US-0591300
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Pred. No. 2.6e-103;
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29-JUL-1998;
24-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human B7.1 co-stimulatory molecule
                                                                                                                                                                                                                                                                                                                                                                                                    These methods can be used for regulating cell growth and division to control disease processes by manipulating mitochondrial metabolism and the expression of cell surface immune proteins. They can be used for treating diseases associated with excessive cellular division, aberrant differentiation, and premature cellular death, e.g. cancers, autoimmune diseases, neurodegenerative disorders etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is human B7.1 co-stimulatory molecule. This is a glycoprotein on the surface of antigen presenting cells. This is involved in stimulation of an immune response by its ability to interact with various immune cell surface receptors. The regulation of cell surface expression of MRC classII and co-stimulatory molecule B7 can be manipulated by regulating the intracellular dissipation of proton motor force which can be assessed in terms of mitochondrial membrane potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         products for treating cancers, autoimmune diseases or neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Newell MK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 115; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of cell surface and membrane characteristics for developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ29320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYVE-) UNIV VERMONT
                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                     147
                                                                                                        121
 207
                                 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                                  Local Similarity
wes 216; Conserv
                                                                                                                                                                                                                              1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-096773/08
                                                                                                                                                                                                             glshfcsgvihvtkevkevatlscghnvsveelagtriywqkekkmvltmmsgdmniwpe 86
                                                                                                                                      yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps 146
                                                                                                                                                          YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                       ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavsskldf 206
                                                                                                                                                                                                                                                                                                                                                                            288 AA;
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0101580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US06874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0082250.
                                                                                                                                                                                                                                                                                                     100.0%; Score 1149; DB 21; 100.0%; Pred. No. 2.6e-103;
                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                         Length 288;
                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                           Gaps
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AAY54920

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the human B7.1 protein sequence.

CC The invention relates to an isolated nucleic acid construct (I)

CC comprising a region encoding an interleakin-12 (IL-12) fusion protein

CC (comprising an IL-12 p35 subunit, an IL-12 p40 subunit and a linker

CC (comprising an IL-12 p35 subunit, an IL-12 p40 subunit and a linker

CC (comprising the subunits) and a region encoding a B7 protein. (I)

CC (comprising the subunits) and a region encoding a B7 protein. (I)

CC (comprising the subunits) and a region encoding a B7 protein. (I)

CC (comprising the subunits) and a region encoding a B7 protein. (I)

CC (comprising the subunits) and a region encoding a B7 protein. (I)

CC (comprising the subunits) and a region encoding a B7 protein. (I)

CC (comprising the subunits) and a region encoding a B7 protein. (I)

CC (comprising the subunits) and a region encoding a B7 protein. (I)

CC (comprising the subunits) and a second either the produced either the functional polypeptide to supplement the patients own.

CC (comprising the subunits) and proteins produced in this way may be used to treat any disease which responds to IL-12 such as tumours

CC (comprising the subunits) and melanomas) and in particular, tumours of the blood cervical tumours and melanomas) and in particular, tumours of the blood such as lambagamia alternativaly, the nolyposities may be used to the sead as
                                                                                                                                                                                                                                                                                                                                                          and the antibodies may be used to detect the presence of IL-12 polypeptides in samples. They may be used diagnostically to quantitate the expression of the polypeptide by patients and hence which subjects
                                                                                                                                                                                                                                                                                                                                                                                                                    such as leukaemia. Alternatively, the polypeptides may be used as antigens in the production of antibodies to IL-12 and to assay for agonists and antagonists of its activity. The antibodies and antagonists may be used to inhibit the activity of IL-12. (I) may also be used diagnostically as a probe which hybridizes to sequences encoding IL-12
                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Fig 10; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid constructs encoding interleukin-12 fusion proteins useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anderson RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;
IL-12 p40 subunit; gene therapy; tumour; leukaemia; B7.1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human B7.1 protein sequence
                                          61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY54920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY54920 standard; Protein; 288 AA
87 yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps 146
                                                                                                      27
                                                                                                                                                                                                                  Local Similarity
                                                                                                             1 GLSHPCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                                                                                                                                                                                            be in need of restorative therapy
                                                                                        glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating leukemia and other cancers -
                                                                                                                                                                                           216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-038261/03.
                                                                                                                                                                                                                                                                                                        288 AA;
                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prentice HG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0751767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0751767
                                                                                                                                                                                                      100.0%; Score 1149; DB 21; Length 288; 100.0%; Pred. No. 2.6e-103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MacDonald ID;
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                                                                                                  composition comprises an allogeneic tumour cell selected from $M620 cell, COLO 205 cell and $M403 cell, and a physiological carrier. The allogeneic cell stimulates an immune response to an autologous tumour cell in the patient. The composition is useful for stimulating an immune response in a patient having an adenocarcinoma. e.g. colon, breast, lung or prostate source of antigen that can be administered to a variety of patients, in contrast to using autologous tumour cells, which must be isolated from each individual patient. The allogeneic cells, which must be isolated from each individual patient. The allogeneic cells are suitable as a cancer vaccine and can stimulate an immune response against suitable as a cancer
                                            vaccine and can stimulate an immune response against autologous tumour cells of a cancer patient. The present sequence represents the amino acid sequence of colorectal tumour antigen CD80 used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                        New composition comprising an allogeneic tumour cell, useful for
stimulating an immune response in a patient having an adenocarcinoma,
especially useful for treating colorectal, breast, lung or prostate
                                                                                                                                                                                                                                                                                            The invention relates to a composition for stimulating an immune response
                                                                                                                                                                                                                                                                              in a patient having an adenocarcinoma or colorectal cancer.
                                                                                                                                                                                                                                                                                                                                        Example 2; Page 130-131; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS11426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KIMM-) KIMMEL CANCER CENT SIDNEY. (IMMU-) IMMUNE RESPONSE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JAN-2000; 2000US-0178498.
28-FEB-2000; 2000US-0185335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colorectal cancer; immunostimulant; cytostatic; immune response; adenocarcinoma; allogeneic tumour cell; SW620 cell; COLO 205 cel SW403 cell; colon; breast; lung; prostate; cancer; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JAN-2001; 2001WO-US02731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour antigen CD80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colorectal tumour antigen CD80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU05121 standard; Protein; 288 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavsskldf 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shawler DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bartholomew RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carlo DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gold DP
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Best Local Similarity Matches 216; Conserv

Conservative

0;

100.0%;

Score 1149; Pred. No. 2 Mismatches

2.6e-103;

Indels Length 288;

0;

Gaps

0

Query Match

Sequence

288 AA;

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RESULT 1
AAB19959
ID AAB1
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      03-NOV-1993;
                      23-SEP-1998;
                                      21-NOV-2000
                                                     US6149905-A
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                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                     metastasis; antitumour; therapy.
                                                                                                                                                                                                                                                                                                                                                             Human; B7; B lymphocyte; antigen; T cell costimulatory molecule; CD28; CTLA4; tumour; melanoma; neuroblastoma; leukaemia; carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                      Human B lymphocyte antigen B7
                                                                                                                                                                                                                                                                                                                                                                                                     19-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB19959 standard; Protein; 288 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {\tt glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE
      93US-0147772
                     98US-0159135
                                                                                                            /note= "/
211..213
                                                                                                                             /note= ",
207..209
                                                                                             /note=
226..2
                                                                                                                                                                                              /note=
53..55
                                                                                                                                                                                                              /note=
139..23
                                                                                                                                                                             /note= "Asn
89..91
                                                                                                                                              186..188
                                                                                                                                                              /note= "Asn is N-glycosylated"
98..100
                                                                                                                                                                                                                                               270..288
                                                                                                                                                                                                                                                                243..269
                                                                                                                                                                                                                                                                                               /label= Signal_peptide
35..288
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                     'note=
                                                                                                                                                                                                                                       'note=
                                                                                                                                                                                                                                                      /note=
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                                                                                    "Asn is N-glycosylated"
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                                                                                                                                    "Asn is N-glycosylated"
                                                                                                                                                                                                     "immunoglobulin C-set domain"
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                                                                                                                                                                                                                                     "intracellular domain"
                                                                                                                                                                                                                                                      "transmembrane domain"
                                                                     "Asn is
                                                                                                                    "Asn is N-glycosylated"
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                                                                   N-glycosylated
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RESULT 11 AAW41415 ID AAW414

AAW41415 standard; Protein; 473

02-JUN-1998

(first entry)

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181

207

NMTTNHSEMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216

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                                                                                                                                                                                                                                                                                                                                                               CC molecule, by using an agent which induces or increases expression
CC of the T cell costimulatory molecule on the tumour cell surface, or
CC by coupling the T cell costimulatory molecule to the tumour cell
CC surface. Tumour cells further modified to express major
CC or in which expression of an MFC associated protein, the invariant
CC cor in which expression of an MFC associated protein, the invariant
CC chain, is inhibited are also disclosed. The modified tumour cells
CC are used to treat a patient with a tumour, preventing or inhibiting
CC metastatic spread or tumour recurrence. The tumour may be a
CC metastatic spread or tumour recurrence. The tumour may be a
CC metastatic spread or tumour by modification of tumour, and a
CC metastating a tumour by modification of tumour cells in vivo
CC are also disclosed. The treatment methods increase the immune period for the tumour cell in vivo. The antitumour T cell mediated immune
CC unmodified tumour cells from which the modified tumour cells and the
CC modified tumour cells is not dependent upon expression of a
CC costimulatory molecule on the tumour cells.
                                                                                                                                                                                                                                                        Best Local Similarity
Matches 216; Conserv
                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell costimulatory molecule that binds to CD28 and CTLA4. Tumour cells modified to express a T cell costimulatory molecule, especially B7, are disclosed. The tumour cells are modified by transfection with a nucleic acid enoding the T cell costimulatory
                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modifying tumor cell for treating tumors, reducing metastatic spread, inhibiting recurrence of tumor and increasing immunogenicity, involves transfecting tumor cells with a nucleic acid encoding B7 molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of human lymphocyte antigen B7, a T cell costimulatory molecule that binds to CD28 and CTLA4. Tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Column 31-34; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEMY ) GENETICS INST INC.
(DAND ) DANA FARBER CANCER INST INC
(HARD ) HARVARD COLLEGE.
    147
                                                                                                                            61
                                                                                                                                                                        27
                                                                                                                                                                                  1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                        YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                     ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
                                                                                                                                                               glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe 86
isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavsskldf
                                                                                yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glimcher LH,
                                                                                                                                                                                                                                                                                                                                                             288 AA;
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Freeman GJ, Ostrand-Rosenberg
                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                        Score 1149; DB 22;
Pred. No. 2.6e-103;
                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                           Length 288;
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                                                                                                                                                                                                                                                    0,
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                                                                                146
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Human B7.1-murine A5B7 F(ab')2 fusion protein

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Best Local
                                                                                                                                                                                                                                                                                                                                               Matches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is the human B7.1-murine A5B7 F(ab')2 fusion protein (AB7), and is an example of the antibody of the invention. The antibody is an anti-CEA (carcinoembryonic antipen) antibody (preferably 806.077 Ab). Host cells or transgenic organisms transformed with DNA encoding the antibody, are used to make the antibody or conjugate. The conjugate is used in a medicament suitable for intravenous administration. The conjugate can be used for cancer therapy, selectively killing tumour cells. The antibody can be used for in vivo or in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-carcinoembryonic antigen antibody 806.077 Ab diagnosis and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-FEB-1997;
04-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reference Example 3; Page 190-193; 208pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copley CG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-CEA antibody;
           hB7.1glu-glu soluble fusion protein
                                                                                    AAW90208 standard; Protein;
                                  10-MAY-1999
                                                                                                                                                  207
                                                                                                                                                                         181
                                                                                                                                                                                                  147
                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                 87
                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                             12
                                                                                                                                                                                                                                                                                                           1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1997-558987/51.
                                                                                                                                                           NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                              YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                                                                                             glshfcsgvihvtkevkevatlscghnvsveelagtriywqkekkmvltmmsgdmniwpe 86
                                                                                                                                                 nmttnhsfmclikyghlrvnqtfnwnttkqehfpdn 242
                                                                                                                                                                                                                                                diagnosis;
                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                          473 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Edge MD,
                                                                                                                                                                                                                                                                                                                                               Conservative
                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97GB-0003103
96GB-0009405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-GB01165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carcinoembryonic antigen; 806.077 Ab; cancer therapy;
                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1149; DB 18; 100.0%; Pred. No. 5.3e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Emery SC
                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                     Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used
                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                  146
                                                                                                                                                                                                                                                                                                                                                0;
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g QΥ

181 147

NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216

is dfeipts nirriic st sggfpephls wlengeel naint tv sqdpetely avs skldfISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180

0

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Дb
                              Qy
                                                              뫄
                                                                                            Qy
                                                                                                                                                                                                                                    This 29 kDa soluble fusion protein, termed hB7.1glu-glu, is composed of human co-stimulatory molecule B7.1 extracellular domain fused C-terminally to a synthetic Glu-glu epitope (see AAW90197). It was produced from total RNA of Epstein-Barr virus-transformed human spleen cells by RT-PCR using primers MR67 and MR145 (see AAW01601). The fusion protein has been produced in Sf9 Spodoptera can be a specific and specific and specific and specific and specific and the furwariant antibodies and small antigen binding peptides which can cross-link, or cross-react with, B7.1 and B7.2 expressed on artigen-specific collection. Methods to produce such antigen-specific collection. Methods to produce such can collection and specific conscious are provided. The molecules are used to treat or prevent diseases of the immune system, in particular graft rejection, graft versus host disease, allergy and autoimmune diseases (claimed).
                                                                                                                               Matches
                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B7 binding molecule; costimulatory molecule; B7.1; CD80; CD86; T cell activation; inhibitor; graft versus host distransplant rejection; allograft rejection; autoimmune disallergy; therapy; human; hB7.1glu-glu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3.1.2; Fig 4; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New molecules which bind B7.1 and B7.2 - useful to prevent and treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-105615/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9858965-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune diseases including allograft rejection
                                                                                                                                               Local Similarity
 87
                                 61
                                                                 27
                                                                             GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE
                                 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                              glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe 86
yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthetic
                                                                                                                                                                                                               251 AA;
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97EP-0870092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-EP03791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35..242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243..251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "human B7.1 (mature protein) extracellular
domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "potential eukaryotic secretory signal
                                                                                                                                               99.7%;
99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lorre K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Glu-Glu detection/purification tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide"
                                                                                                                                               Score 1146; DB 20;
Pred. No. 4.2e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sablon
                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   versus host disease; autoimmune disease;
                                                                                                                                   Indels
                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B7.2;
                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      composed
                                                                                                                                 Gaps
                                                                                                   60
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RESULT 1
AAW86004
ID AAW8
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                                                                                                                                                                                                                                Matches 215;
          AAW86004 standard;
                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                   New xanthene derivatives useful as immunomodulators - e.g. methyl 2-(carboxymethylsulphinyl)-5,7-dichloro-3,8-dihydroxy-6-methyl-9-oxo-9H-xanthene-1-carboxylate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-1996;
05-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP795554-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening; inhibitor; enhancer; binding; CD28; B7-1; soluble B7-1-Ig; immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW38415 standard;
                                                                                                                                                                                                                                                                                                       ç
                                                                                                                                                                                                                                                                                                               The present sequence was used in the development of a novel for screening for compounds that inhibit or enhance binding
                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 6 and 7; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-SEP-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soluble B7-1-Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW38415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207
                                                              207
                                                                                  181
                                                                                                       147
                                                                                                                           121
                                                                                                                                              87
                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                  61
                                                                                                                                                                                       27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE
                                                                                                                                                                                                                                                                                                        B7-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nmttnhsfmclikyghlrvnqtfnwnttkqehfpdh 242
                                                                                 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                              ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
                                                                                                                                             YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                                                                                                                                                                                                                       1997-450803/42.
                                                                                                     isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavsskldf
                                                                                                                                                                                     glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe
                                                                                                                                                                                                                                                                                  475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hida
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96JP-0262085
96JP-0047795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97EP-0301438
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ή
          Protein; 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                       99.6%; Score 1144; DB 18; 99.5%; Pred. No. 1.6e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Kurokawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  475
                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ĄΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakanishi
                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                method
of CD28
                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                             Gaps
                                                                                                                                             146
                                                                                                                                                                                      86
                                                                                                                                                                                                          60
                                                                                                                                                                                                                              0;
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δã
                              Db
                                                                                                                                                                      Comprising the amino acid sequence of B7-1.574.1, a fusion protein comprising the extracellular domain (amino acids 1-215) of human co-stimulatory molecule B7-1 joined via a flexible peptide linker to an scFv (see AAM86002) derived from murine 574 monoclonal antibody. B7-1.574.1 cDNA (see AAW80292) can be inserted into vector pCI to allow expression of the fusion protein in mammalian cells. The trophoblast cell surface antigen defined by 574 is expressed at high levels on the cells of a wide variety of human tumours. The invention relates to a vector comprising a nucleotide sequence coding for a tumour interacting protein (TIP) and optionally a nucleotide sequence of interest (NOI) which encodes a protein of interest (POI), the vector being capable of delivering the NOI cand/or POI to the tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The vector is used to treat cancer, and may also used as a gene delivery system for introducing at least 1 gene encoding a TIP (preferably a tumour binding protein) into a haematopoietic cell lineage. B7-1 is expected to bind specifically to CD28 and CTLA-4 present on human T-cells.
                                                                                            Matches
                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JUL-1997;
04-JUN-1997;
20-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New vector encoding a tumour interacting protein for treating cancer contains a desired nucleotide sequence and/or protein which recognises tumours, and is used as a gene delivery system to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen; monoclonal antibody; single chain antibody; mouse; human; B7-1; co-stimulatory molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric -
Chimeric -
                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV80292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bebbington CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric - synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human B7-1.5T4.1 protein fusion,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5; Fig 2; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-059910/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9855607-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW86004;
 61
                              27
                           YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS
                                                                                            215;
                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus sp.
Homo sapiens.
                                                                                                                                                                      488 AA;
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97GB-0014230.
97GB-0011579.
97GB-0013150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOMEDICA UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-GB01627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carroll MW,
                                                                                                       99.5%;
                                                                                                       Score 1143; DB 20; Pred. No. 2.1e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTD.
                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ellard FM,
                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specific for human 5T4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kingsman
                                                                                         0;
                                                                                                                      Length 488;
                                                                                           Indels
                                                                                         0;
                                                                                         Gaps
                              86
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87

yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
AAB83836
                                            The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treatment of treatment of your diseases including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system disorders autoimmune diseases, cancers, central nervous system disorders of including Parkinson's disease, periodontal diseases, cardiopulmonary confections, diabetes, Helicobacter-related diseases, and other immune constructers. The present sequence represents a B7-1.574.1 fusion protein. This comprises the N-terminus of the 574 ScFv is fused after amino acid
                                                                                                                                                                                                                                                                                                                                       Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-1999; 99WO-GB03859.
15-FEB-2000; 2000GB-0003527.
02-MAR-2000; 2000GB-0005071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single chain antibody; ScFv; inflammatory disease; arthritis; cancer; hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder.
Sequence
                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                             molecule
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-343805/36.
N-PSDB; AAF89730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-2000; 2000WO-GB04317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB83836 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kingsman A, Kingsman SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of a B7-1.5T4.1 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                  of human
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Best Local
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                                                                                                                                                                                           Local Similarity
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                                                      ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF
                                                                                       YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE
nmttnhsfmclikyghlrvnqtfnwnttkqehfpd
                       NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPD
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                                                                                                                                                                                         99.5%;
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                                                                                                                                                                                         Score 1143; DB 22;
Pred. No. 2.1e-102;
                                                                                                                                                                                 Mismatches
  241
                                                                                                                                                                                                     Length 488;
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                                             206
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Search completed: June 18, 2002, 11:44:32 Job time: 85 sec

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
/cgn2_6/ptodata/2/paa/US085_COMB.pep:*
/cgn2_6/ptodata/2/paa/US086_COMB.pep:*
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/cgn2_6/ptcdata/2/paa/US06_COMB.pep:*
/cgn2_6/ptcdata/2/paa/US07_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	:	1	ength	BB	ID	Description
1	1149		216	æ	US-08-459-766B-8	Sequence 8, Appli
2	1149	100.0	216	19	US-09-569-164A-8	Sequence 8, Appl:
ω	1149	100.0	226	Ľ	PCT-US01-41430-21	Sequence 21, Appl
4	1149	100.0	248	Н	PCT-US01-06769-12	Sequence 12, Appl
σ	1149	100.0	288	1	PCT-US01-41430-15	Sequence 15, Appl
თ	1149	100.0	288	ω	US-07-751-306C-2	Sequence 2, Appli
7	1149	100.0	288	σ	US-08-109-393A-29	Sequence 29, Appl

ALIGNMENTS

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US-08-459-766B-8

Sequence 8, Application US/08459766B

Sequence 8, Application US/08459766B

Sequence 8, Application US/08459766B

GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Linsley, Peter S.
APPLICANT: Damle, Nitin K.
CURRENT APPLICATION NUMBER: US/08/459,766B

CURRENT APPLICATION NUMBER: US/08/459,766B

CURRENT FILING DATE: 1990-03-26

PRIOR APPLICATION NUMBER: 07/547,980

PRIOR APPLICATION NUMBER: 07/547,980

PRIOR FILING DATE: 1990-07-02

PRIOR APPLICATION NUMBER: 07/722,101

PRIOR APPLICATION NUMBER: 07/722,101

PRIOR APPLICATION NUMBER: 08/219,200

PRIOR APPLICATION NUMBER: 09/547,980

PRIOR APPLIC
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US-09-569-164A-8
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PRIOR FILING DATE: 1990-07-02
PRIOR PRIOR PRICATION NUMBER: 07/72,101
PRIOR FILING DATE: 1991-06-27
PRIOR APPLICATION NUMBER: 08/219,200
PRIOR FILING DATE: 1994-03-29
PRIOR FILING DATE: 1994-03-29
PRIOR APPLICATION NUMBER: 08/459,766
PRIOR FILING DATE: 1995-06-02
                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Pat
SEQ ID NO 8
LENGTH: 216
                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Freedman, Gordon J.
AUTHORS: Freedman, Arnold S.
AUTHORS: Segil, Jeffrey M.
AUTHORS: Lee, Grace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09569164A GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                     AUTHORS: Whitman, James F.
AUTHORS: Nadler, Lee M.
TITLE: B7, A NEW MEMEBER OF THE IG
TITLE: EXPRESSION ON ACTIVATED AND
                     ISSUE: 8
PAGES: 2714-2722
DATE: 1989-10-15
                                                                                  JOURNAL: J. Immunol. VOLUME: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAGES: 2714-2722
DATE: 1989-10-15
RELEVANT RESIDUES: 1 TO 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS: Lee, Grace
AUTHORS: Whitman, James F.
AUTHORS: Whitman, James F.
TITLE: B7, A NEW MEMBER OF THE 19 SUPERFAMILY WITH UNIQUE
TITLE: EXPRESSION ON ACTIVATED AND NEOPLASTIC B CELLS
RELEVANT RESIDUES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISSUE: 8
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  1 TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-05-11
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                                                                                                                         SUPERFAMILY WITH UNIQUE NEOPLASTIC B CELLS
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Sequence 12, Application PC/TUS0106769
GENERAL INFORMATION:
APPLICANT: Mayo Medical Ventures
APPLICANT: Mayo Medical Ventures
OF INVENTION: hB7-H2, A NOVEL CO-STIMULATORY MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LEUGTH: 226
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application PC/TUS0141430
GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education and Research
TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
TITLE OF INVENTION: MOLECULES
FILE REFERENCE: 07039-219W01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 216;
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/220,991
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: PCT/US01/41430 CURRENT FILING DATE: 2001-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                               191
                                                                                                                                                                                                                     181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                    121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GLSHECSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                           YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 130
                                                                                                                                                                                                                                                           ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1149; DB 1; 100.0%; Pred. No. 6.8e-112; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1149; DB 19; 100.0%; Pred. No. 6.4e-112; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 226;
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FILE REFERENCE: 07039-202WO1

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207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-06769-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application PC/TUS0141430
GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education and Research
TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
TITLE OF INVENTION: MOLECULES
FILE REFERENCE: 07039-219W01
CURRENT APPLICATION NUMBER: PCT/US01/41430
CURRENT APPLICATION NUMBER: 60/220,991
PRIOR APPLICATION NUMBER: 60/220,991
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 288
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Best Local :
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Best Local S
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CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/186,519
PRIOR FILING DATE: 2000-03-02
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                        147
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                                                                                                                                                                                                                                                                                  Local Similarity
hes 216; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS
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                                                                                                                                                                                                          GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86
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                                                                                                                                                      YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146
                                                        ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF
                                                                                                                                                                                                                                                                                    100.0%; Score 1149; DB 1; ilarity 100.0%; Pred. No. 9.7e-112; Conservative 0; Mismatches 0;
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 Mismatches

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RESULT 6
US-07-751-306C-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/591,300
FILING DATE: 01-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: HART, JULIA D.
REGISTRATION NUMBER: 3312
REFERENCE/DOCKET NUMBER: DFCI-116.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255-8900
TELEPHONE: (203) 255-8900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (203) 259-284
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: DNA Enc
TITLE OF INVENTION: Of The
TITLE OF INVENTION: Activat
NUMBER OF SEQUENCES: 4
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APPLICANT: FREEDMAN, ARNOLD S.
APPLICANT: NADLER, LEE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect 5.0 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                               FEATURE:
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CITY: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Disk
COMPUTER: IBM Per
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: UZIP: 02115
                                                                                                                                                                                     NAME/KEY: transmembrar LOCATION: 209 to 235 IDENTIFICATION METHOD: IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                           NAME/KEY: extracellula LOCATION: 1 to 208 IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION METHOD: amino terminal sequencing IDENTIFICATION METHOD: soluble protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: signal sequence LOCATION: -34 to -1
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FILING DATE: 19910828
                   NAME/KEY: N-linked glycosylation LOCATION: 19 to 21
                                                                                                  IDENTIFICATION METHOD:
                                                                                                                        NAME/KEY: intracellular domain LOCATION: 236 to 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                   IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
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AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                       extracellular domain
                                                                                                                                                                                                                                                  transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259-2846
ID NO: 2:
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similarity with known
                                                                                sequence
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                                                                                                                    Query Match
Best Local
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61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                               ISSUE:
PAGES:
                                                                                                                                                                                                                                                                             AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
                                     27
                                                                                                                    Local Similarity
                                                                                                                                                                                                DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION METHOD: IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Ig C-set domain LOCATION: 105 to 202
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                                AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS:
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                                                                                                                                                                                                                                    2714-2722
                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                              SEGIL, JEFFREY M.
LEE, GRACE
                                                                                                                                                                                                                                                                                                                                                                                                          FREEMAN, GORDON J.
                                                                                                                                                                                                                                                                                                                                                                                              FREEDMAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-linked glycosylation 64 to 66
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177 to 179
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                                                                                                  0;
                                                                                                Score 1149; DB 3;
Pred. No. 9.7e-112;
; Mismatches 0;
                                                                                                                                                                                                  2: From -26 to
                                                                                                Indels
                                                                                                                              Length
                                                                                                                                  288;
                                                                                                  0;
                                                                                              Gaps
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RESULT 7
US-08-109-393A-29
; Sequence 29, Application US/08109393A
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: RP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JUL-1993
ATTORNEY_AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Freeman, Gordon APPLICANT: Nadler, Lee M. APPLICANT: Grav. Gary S.
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                    FEATURE:
                                                                                                                                                                                   FEATURE:
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DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gray, Gary S.
TITLE OF INVENTION: Novel CTLA4/CI
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                   NAME/KEY: transmembrane domain LOCATION: 209 to 235 IDENTIFICATION METHOD: similar
                                                                                                                                                                                                                                                                                                                       DIECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                  NAME/KEY: signal sequence LOCATION: -34 to -1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19
CLASSIFICATION:
  IDENTIFICATION METHOD:
                                                             NAME/KEY:
                                                                                                                                                                                                       OTHER INFORMATION:
                                                                                                                                                                                                                       IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87
                                                                                                   IDENTIFICATION METHOD:
                                                                                                                        IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                          288 amino acids
                                                                                                                                                            extracellular domain
                                                                                                                                             1 to 208
                                                                                                                                                                                                                                                                                                                                                                                      linear
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19-AUG-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel CTLA4/CD28 Ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gordon J.
                                                                                                                                                                                                       hydrophobic
                                                                                                                                                                                                                       amino terminal sequencing soluble protein
similarity with known sequence
                                                                                                 similarity with known sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPI-004CP
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; DATE: 15-OCT-1989
; RELEVANT RESIDUES IN SEQ
US-08-109-393A-29
                                                                                                                                                                                                                                                               NAME/KEY: IG C-set domain LOCATION: 105 to 202 IDENTIFICATION METHOD: SITUALITY OF THE PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                 JOURNAL: 11.
                                                                                                   AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplast:
JOURNAL: The Journal of Immunology
                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: IG V-set dor
LOCATION: 1 to 104
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: intracellular domain LOCATION: 236 to 254 IDENTIFICATION METHOD: similar:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 198 to 200 IDENTIFICATION METHOD: IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: N-linked glycosylation LOCATION: 152 to 154 IDENTIFICATION METHOD: similarit. IDENTIFICATION METHOD: sequence
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                                                   2714-2722
                                                                                                                                                                                                                                FREEDMAN, ARNOLD S.
                                                                                                                                                                                            SEGIL, JEFFREY M.
LEE, GRACE
                                                                                                                                                                                                                                                                                                                                                                                                              Ig V-set domain 1 to 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-linked glycosylation
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19 to 21
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                    -26
                                                                                                                        Neoplastic B Cells
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                                                                                                                                                      ; TOPOLOGY: 1i; MOLECULE TYPE: US-08-147-773-6
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                                                                   Query Match
Best Local Similarity
Matches 216; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.0%; Pred. No. 9.7e-112; Matches 216; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                        TELEFAX: (617) 227-594
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/10,393;
APPLICATION NUMBER: 19-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
                                                                                                                                                                                                                                                                                                                        NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,20
REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
   27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE
                                 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE
YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02109
                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 State Street, Suite 510
                                                                                                                                                                                                                        288 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                   Conservative
                                                                                                                                                                                       linear
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                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                           227-5941
                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                                            36,207
                                                                                                                                                                                                                                                           6.
                                                                   0;
                                                                                                                                                                                                                                                                                                                             RPI-008
                                                                   Score 1149; DB 5;
Pred. No. 9.7e-112;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 29
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APPLICANT: 1
APPLICANT: 0
APPLICANT: 0
                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624; 08/109,393; 08/147,773
APPLICATION NUMBER: 26-JUL-1993; 19-AUG-1993; 03-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Novel CTLA4/CITITLE OF INVENTION: Uses Therefor NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: prof
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
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                                                                                                                                               OTHER INFORMATION:
                                                                                                                                                                 IDENTIFICATION METHOD: amino terminal sequencing of IDENTIFICATION METHOD: soluble protein
                                                                                                                                                                                                                    NAME/KEY: signal sequence
                                                                                                                                                                                                                                                              DESCRIPTION:
                 NAME/KEY:
                                                                                                                                                                                                        LOCATION:
LOCATION:
                                                    IDENTIFICATION METHOD:
                                                                         IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                DESCRIPTION:
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Nadler, Lee M.
Gray, Gary S.
Greenfield, Edward
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transmembrane domain 209, to 235 '
                                                                                         extracellular domain 1 to 208
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B cell activation antigen; natural ligand
for CD28 T cell surface antigen; transmembrane protein
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; ISSUE: 8
; PAGES: 2714-2722
; DATE: 15-OCT-1989
; RELEVANT RESIDUES IN US-08-280-757-29
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NAME/KEY: IG V-set doma
LOCATION: 1 to 104
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD: Sequ
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
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NAME/KEY: N-linked glycosylation LOCATION: 192 to 194
IDENTIFICATION METHOD: similarit
                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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LOCATION:
                                                                                      JOURNAL: VOLUME:
                                                                                                                                        AUTHORS:
TITLE: I
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LOCATION: 177 to 179
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                           AUTHORS:
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B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplast
                                                                                                                                                                                        FREEDMAN, ARNOLD S. SEGIL, JEFFREY M. LEE, GRACE
                                                                                                    The Journal of Immunology
                                                                                                                                                                        WHITMAN,
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1 to 104
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177 to 179
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GENERAL INFORMATION:
APPLICANT: June, Carl H.
APPLICANT: Thompson, Craig B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 216;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,816A
FILING DATE: May 4, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,253
FILING DATE: 10 MARCH 1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
CITY: BO:
STATE: M:
COUNTRY:
ZIP: 021:
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                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/864,805 FILING DATE: 7 APR 1992 APPLICATION NUMBER: US 08/247,505 FILING DATE: 23 MAY 1994
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APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
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                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 199
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nabel, Gary J
Gray, Gary S.
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May 4, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO:
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NAME/KEY:
LOCATION:
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LOCATION:
                                                                                                            IDENTIFICATION METHOD: IDENTIFICATION METHOD: FEATURE:
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REGISTRACION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                     NAME/KEY: N-linked gly LOCATION: 192 to 194 IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION METHOD: amino terminal sequencing IDENTIFICATION METHOD: soluble protein OTHER INFORMATION: hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: N-linked glycosylation IOCATION: 55 to 57 IDENTIFICATION METHOD: similarit IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: intracellular domain LOCATION: 236 to 254 IDENTIFICATION METHOD: similar
                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD: IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: N-linked glycosylation LOCATION: 152 to 154
                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTIFICATION METHOD:
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   NAME/KEY:
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amino acid
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173 to 175
                                                                                       N-linked glycosylation
                                                                                                                                                                 N-linked glycosylation 177 to 179
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N-linked glycosylation
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B cell activation antigen; natural ligand
for CD28 T cell surface antigen; transmembrane
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                                                                                                                                            similarity with known
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                                                                                                                                                                                                                         Sequence 2, Application
GENERAL INFORMATION:
APPLICANT: FREEMAN
APPLICANT: FREEDMAN
APPLICANT: NADLER,
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                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 216; Conserv
               ZIP: 02115
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD: PUBLICATION INFORMATION:
                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                             147
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                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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AUTHORS:
AUTHORS:
                                                                               CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAGES:
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VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS:
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 COMPUTER:
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IDENTIFICATION
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                                                                                                                                                                                                                                                                                                                                                                           NMTTNHSFMCLIKYGHLRVNOTFNWNTTKQEHFPDN 216
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15-OCT-1989
                                                                                                  Boston
                                                                                                                                                                                                                                                                                             Application US/08453386
                                                              Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FREEMAN, GORDON J. FREEDMAN, ARNOLD S. SEGIL, JEFFREY M. LEE, GRACE
                                                                                                             44 Binney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                            FREEMAN, GORDON J. FREEDMAN, ARNOLD S.
                                                                                                                                                                                                                           NADLER, LEE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Journal of Immunology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig C-set domain
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1 to 104
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3: Diskette, 3.50 inch, 720kb storage
IBM Personal*System 2; Model 30
                                                                                                                              The Dana-Farber Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to 200 METHOD:
                                                                                                                                                                              DNA Encoding B7, A New Member Of The IgG Superfamily With Unique Expression Activated And Neoplastic B Cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1149; DB 8; 100.0%; Pred. No. 9.7e-112; tive 0; Mismatches 0;
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TELEFAX: (203) 259-2846
INFORMATION FOR SEQ ID NO: 2:
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NAME/KEY:
LOCATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255-8900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: HART, JULIA D.
REGISTRATION NUMBER: 331
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PRIOR APPLICATION DATA:
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LOCATION:
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LOCATION:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: intracellula LOCATION: 236 to 254 IDENTIFICATION METHOD: IDENTIFICATION METHOD:
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IDENTIFICATION METHOD: IDENTIFICATION METHOD:
                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                       NAME/KEY: N-linked glycosylation LOCATION: 64 to 66 IDENTIFICATION METHOD: similarit
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SOFTWARE: WordPer
                                                                                     IDENTIFICATION METHOD:
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                                                                                                       IDENTIFICATION METHOD:
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WordPerfect 5.0
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19 to 21
                                N-linked glycosylation
173 to 175
                                                                                                                       N-linked glycosylation
152 to 154
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UMBER: US 07/591,300
01-OCT-1990
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B cell activation antigen; natural ligand
for CD28 T cell surface antigen; transmembrane protein
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                                                                                                                                                           US-08-453-386A-2
Sequence 2, Application US/08453386A
GENERAL INFORMATION:
APPLICANT: FREEDMAN, Gordon J.
APPLICANT: FREEDMAN, AINOID S.
APPLICANT: NADLER, Lee M.
TITLE OF INVENTION: DNA Encoding B7, A New
TITLE OF INVENTION: With Unique Expression
TITLE OF INVENTION: Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                             181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                        207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplast:
JOURNAL: The Journal of Immunology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: IG V-set domain LOCATION: 1 to 104 IDENTIFICATION METHOD: sin IDENTIFICATION METHOD: see
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                                                                                                                                                                                                                                                                                                                                                                                               87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS
                                                                                                                                                                                                                                                                                                                                                                                                                61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAGES: 2714-2722
DATE: 15-OCT-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
                                                                                                                                                                                                                                                                                                                                        ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSODPETELYAVSSKLDF 180
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LEE, GRACE
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                    Member Of The IgG Superfamily On Activated And Neoplastic
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PRIOR APPLICATION NUMBER: 08/15:
PRIOR FILING DATE: 1993-11-15
PRIOR APPLICATION NUMBER: 07/751
PRIOR FILING DATE: 1991-08-28
PRIOR FILING DATE: 1990-01-10
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 288
TYPE: PRT
TYPE: PRT
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; PAGES: 2714-2722
; DATE: 15-OCT-1989
US-08-453-386A-2
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LOCATION: (35)
NAME/KEY: DOMAIN
LOCATION: (1)..(208)
OTHER INFORMATION: Extracellular
NAME/KEY: TRANSMEM
LOCATION: (209)..(235)
NAME/KEY: TRANSMEM
LOCATION: (209)..(235)
NAME/KEY: DOMAIN
LOCATION: (236)..(254)
COPHER INFORMATION: N-linked glycosylation at OTHER INFORMATION
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CURRENT FILING DATE: 1995-05-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: DOMAIN
LOCATION: (105)...(202)
OTHER INFORMATION: Ig C-set
OTHER INFORMATION: Description of Artificial Sequence: Primer
OTHER INFORMATION: Signal sequence from positions -34 through
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LOCATION: (1)..(104)
OTHER INFORMATION: IG V-set
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                          181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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cal Similarity 100.0%;
216; Conservation
                                                                                                                     ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN
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Pred. No. 9.7e-112;
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LOCATION: 1 to 208

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US-08-592-711-2
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ETLING DATE: 26-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/43
APPLICATION NUMBER: US 08/40
APPLICATION NUMBER: US 08/40
FILING DATE: 10-MARCH-1995
APPLICATION NUMBER: US 08/25
APPLICATION NUMBER: US 08/25
APPLICATION NUMBER: US 08/25
ETLING DATE: 3-JUNE-1994
FILING DATE: 3-JUNE-1994
                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acid
                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 23-NOV-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 07
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08
FILING DATE: 25-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
                  FEATURF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US 07/275,433
TITING DATE: 23 NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07 FILING DATE: 7-APR-1992 APPLICATION NUMBER: US 08 FILING DATE: 23-MAY-1994
                                        OTHER INFORMATION:
                                                      IDENTIFICATION METHOD: amino terminal sequencing of IDENTIFICATION METHOD: soluble protein
                                                                                                     LOCATION:
                                                                                                                                                                DESCRIPTION:
                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US (FILING DATE: 7-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 4-JUNE-1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME/KEY: extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                      NAME/KEY: signal sequence
                                                                                                                                                                                     DESCRIPTION:
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                                                                                                                                                                                                                                                                 288 amino acids
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                                                                                                                                                                                                                           linear
                                                                                                     -34 to -1
                                                                                                                                                   protein
B cell activation antigen; natural ligand
for CD28 T cell surface antigen; transmembrane protein
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                                        hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 07/864,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 07/864,866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                us 07/902,467
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IDENTIFICATION METHOD: PUBLICATION INFORMATION:
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                   AUTHORS:
TITLE: E
TITLE: U
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LOCATION:
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LOCATION:
                                                                                                               AUTHORS:
                                                                                                                                 AUTHORS:
                                                                                                                                                                                                                                         IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: N-linked glycosylation LOCATION: 198 to 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: N-linked gl:
LOCATION: 177 to 179
IDENTIFICATION METHOD:
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LOCATION: 152 to 154
    JOURNAL:
                                                                   AUTHORS:
                                                                                   AUTHORS:
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                                                                                                                                                                              IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                        LOCATION:
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3: NADLER, LEE M.

B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells
: The Journal of Immunology
                                                                              SEGIL, JEFFREY M.
LEE, GRACE
                                                              WHITMAN,
                                                                                                              FREEDMAN, ARNOLD S.
                                                                                                                             FREEMAN, GORDON J.
                                                                                                                                                                                         Ig C-set domain
105 to 202
                                                                                                                                                                                                                                                                       Ig V-set domain 1 to 104
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177 to 179
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                                                                JAMES F.
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PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: US-08-592-711-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                           ATTORNEY/AGENT INFORMATION:
NAME: MANDIAGOURAS, ANY E.
REGISTRATION UNMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
                                                          TELEFAX: (617) 227-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3
TITLE OF INVENTION: WITH INCREASED IMMUNOGENICITY AND USES THEREFO
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
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CITY: B
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                                                                                                                                                                                                                APPLICATION NUMBER: 08/456,104
FILING DATE:
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JUL-1993
APPLICATION NUMBER: 08/109,393
APPLICATION NUMBER: 19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27
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                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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Pred. No. 9.7e-112;
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APPLICANT: Newell, Martha K.

TITLE OF INVENTION: METHODS AND PRODUCTS RELATED TO TITLE OF INVENTION: METHODS AND PRODUCTS RELATED TO TITLE OF INVENTION: METHODS IN DISEASE FILE REFERENCE: V0139/7028/HK

CURRENT APPLICATION NUMBER: US/09/277,575

CURRENT FILING DATE: 1999-03-26

EARLIER APPLICATION NUMBER: US. 60/082,250

EARLIER FILING DATE: 1998-04-17

EARLIER FILING DATE: 1998-07-29

EARLIER FILING DATE: 1998-07-29

EARLIER FILING DATE: 1998-07-29

EARLIER APPLICATION NUMBER: U.S. 60/101,580

EARLIER APPLICATION NUMBER: U.S. 60/101,580
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                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09277575 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 1149; DB 16; Best Local Similarity 100.0%; Pred. No. 9.7e-112;
                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 288
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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                               181
                                                               147
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                                                                                                                                 Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKWVLTMMSGDMNIWPE 60
                                                              ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
               NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                   GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
                                                                                                                                                                                                                                                                     216;
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Search completed: June 18, 2002, 11:46:50 Job time: 223 sec

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Result
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Maximum Match 10
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Maximum DB seq length: 2000000000
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       score greater than or equal to the score of the result beir
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Gapop 10.0 , Gapext 0.5
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Listing first 45 summaries
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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    US-08-153-262-2

US-08-280-75/B-29

US-08-280-75/B-29

US-08-205-65/PA-19

US-08-205-65/PA-19

US-08-403-253A-2

PCT-US95-025/6-19

US-09-460-384-36

US-09-460-384-36

US-09-460-384-36

US-08-30-172-15

US-08-30-172-15

US-08-30-172-17

US-08-30-172-17

US-08-30-172-17

US-08-205-65/PA-17

US-08-205-65/PA-2

US-08-103-65/PA-2

US-08-103-65/PA-2
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US-08-456-104-6
US-08-101-624-23
US-08-751-767A-6
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Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 65, Appl	Sequence 65, Appl	Sequence 63, Appl	Sequence 63, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 9, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 31, Appl	Sequence 31, Appl

ALIGNMENTS

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; Sequence 2, Application US/08147772
Patent No. 5858776
; GENERAL INFORMATION:
APPLICANT: Ostrand-Rosenberg, Suze APPLICANT: Baskar, Sivasubramaniar APPLICANT: Glimcher, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
US-08-147-772-2
                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RP
                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
NUMBER OF SEQUENCES: 4
                                                                           MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                FEATURE:
                                                                                                                                              TYPE: amin
TOPOLOGY:
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                      NAME/KEY: signal sequence LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 State Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baskar, Sivasubramanian
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                                                                                                                                                linear
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                                                                                  antigen; transmembrane protein
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                                                                                                                                                                                                                                                                                        NAME/KEY: N-linked glycosylation LOCATION: 198 to 200 IDENTIFICATION METHOD: similarit. IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: N-linked glycosylation LOCATION: 192 to 194 IDENTIFICATION METHOD: similarit
                                                                         AUTHORS:
                                                                                                        IDENTIFICATION METHOD: IDENTIFICATION METHOD:
                                                                                                                                                                                                 NAME/KEY: IG V-set domain LOCATION: 1 to 104 IDENTIFICATION METHOD: sin IDENTIFICATION METHOD: sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 177
IDENTIFICATION
                    AUTHQRS:
                                       AUTHORS:
                                                      AUTHORS:
                                                                                                                                            NAME/KEY: Ig C-set domain LOCATION: 105 to 202
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IDENTIFICATION METHOD:
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                 FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
WHITMAN, JAMES F.
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173 to 175
TION METHOD: similarit
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RESULT 2
US-08-456-104-6
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                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/101,624;

FILING DATE: 26-JUL-1993;

APPLICATION NUMBER: 08/109,393;

APPLICATION NUMBER: 19-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: MANDER: 36,207

REGISTRATION NUMBER: 36,207
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Best Local Similarity
Matches 216; Conserv
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               TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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ADDRESSEE: LAHIVE & COCKFIELD
                                                              REFERENCE/DOCKET NUMBER: RP TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS
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TITLE: E
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DATE: 15-OCT-1989
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CHARACTERISTICS:
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B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplast.
L: The Journal of Immunology
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TYPE: amino acids; TYPE: amino acids; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-456-104-6
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                                                                  TELEPHONE: (617) 227-7400
TELERAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY.
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APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 5942607el CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/101,624
FILING DATE: 26-JUL-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                           MOLECULE TYPE:
DESCRIPTION:
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STATE: Massa
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          DESCRIPTION:
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protein
B cell activation antigen; natural ligand
for CD28 T cell surface antigen; transmembrane protein
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LOCATION: 105 to 202
IDENTIFICATION METHOD: simil
IDENTIFICATION METHOD: seque.
PUBLICATION INFORMATION:
AUTHORS: FREFMAN
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LOCATION:
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                                                                                                                         NAME/KEY: IG V-set domain LOCATION: 1 to 104 IDENTIFICATION METHOD: sin IDENTIFICATION METHOD: sec
                                                                                                                                                                                                                                                                                                            NAME/KEY: N-linked glycosylation LOCATION: 192 to 194 IDENTIFICATION METHOD: similarit
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LOCATION: 173
IDENTIFICATION
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198 to 200
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177 to 179
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173 to 175
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19 to 21
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RESULT 4
US-08-751-767A-6
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APPLICANT: ANDERSON, ROBERT J.
                                 TELEFAX: 7038164100 INFORMATION FOR SEQ ID NO: 6:
                                                REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEPAX: 7038164100
                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN NUMBER OF SEQUENCES: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
                SEQUENCE CHARACTERISTICS: >
                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: SADOFF, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 23: From -26 to 262
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B7, A New Member Of The Ig Superfamily With
B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells
L: The Journal of Immunology
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1100 NORTH GLEBE ROAD
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WHITMAN, JA
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                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; score 1149; DB 2; 100.0%; Pred. No. 5.2e-113; 7ative 0; Mismatches 0;
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Patent No. 6071716
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                                                                                                                                        TELEFAX: (203) 259-28 INFORMATION FOR SEQ ID NO:
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                     MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: HART, JULIA D.
REGISTRATION NUMBER: 33132
REFERENCE/DOCKET NUMBER: DFCI-116.1
                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: MS/DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
                                                                                                 SEQUENCE CHARACTERISTICS: LENGTH: 288 amino acids
                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskett
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                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP:
                                                                                     TYPE:
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/751,306 FILING DATE: 28-AUG-1991
                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/153,262
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                                                                                                                                                                              TELEPHONE:
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                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Diskette, 3.50 inch, 720kb storage IBM Personal System 2; Model 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Dana-Farber Cancer Institute
                                                                                                                                                                              (203)
protein

B cell activation antigen; natural ligand for CD28 T cell surface antigen; transmem
                                                                                                                                                          259-2846
                                                                                                                                                                            255-8900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Encoding B7, A New Member Of The IgG Superfamily With Unique Expression On Activated And Neoplastic B Cells.
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   transmembrane protein
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NAME/KEY: Ig C-set domain LOCATION: 105 to 202 IDENTIFICATION METHOD: similarii IDENTIFICATION METHOD: sequence PUBLICATION INFORMATION:
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NAME/KEY:
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LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: transmembrane domain COCATION: 209 to 235 IDENTIFICATION METHOD: similar: IDENTIFICATION METHOD: sequence
                                                                                                                                               NAME/KEY: IG V-set domain LOCATION: 1 to 104 IDENTIFICATION METHOD: sin
                                                                                                                                                                                                                                            NAME/KEY: N-linked glycosylation LOCATION: 198 to 200 IDENTIFICATION METHOD: similarit
                                                                                                                                                                                                                                                                                                                                           NAME/KEY: N-linked glycosylation LOCATION: 192 to 194 IDENTIFICATION METHOD: similarit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: N-linked glycosylation LOCATION: 173 to 175 IDENTIFICATION METHOD: similarity IDENTIFICATION METHOD: sequence
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LOCATION:
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FREEMAN, GORDON J.
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19 to 21
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                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,7447
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/280,757
APPLICATION NUMBER: 08/280,757
FILING DATE: 26-JUL-1994
FILING DATE: 26-JUL-1994
FILING DATE: 26-JUL-1994
FILING DATE: 26-JUL-1994
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APPLICANT: Freeman, Gordon ...
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
TITLE OF SECUENCES: 55
                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
           APPLICATION NUMBER: 08/10
FILING DATE: 28-AUG-1993
APPLICATION NUMBER: 08/10
FILING DATE: 26-JULY 1993
APPLICATION NUMBER: 08/14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147
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AUTHORS:
AUTHORS:
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                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                     STREET: 60 S
CITY: Boston
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                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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DATE: 15-OCT-1989
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                                                                                                                                                                                                                                                                                                                                                       STATE:
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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S: SEGIL, JEFFREY M.
S: LEE, GRACE
S: WHITMAN, JAMES F.
S: NADLER, LEE M.
B7, A New Member Of The Ig Superfamily With Unique Expression On Activated And Neoplastic L: The Journal of Immunology
                                                                                                                                                                                                                                                                                                                                                       Massachusetts
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                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
                             26-JULY-1993
3-NOV-1993
                                              08/101,624
                                                                                                                                                                                           US/08/479,744A
             08/147,773
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Pred. No. 5.2e-113;
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TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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NAME/KEY: signal sequence
LOCATION: -34 to -1
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DESCRIPTION:
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                                    NAME/KEY: N-linked glycosylation LOCATION: 192 to 194 IDENTIFICATION METHOD: similarit IDENTIFICATION METHOD: sequence
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                                                                                                                                                                    NAME/KEY: N-linked glycosylation LOCATION: 177 to 179
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LOCATION:
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NAME/KEY: N-linked glycosylation
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amino acid
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55 to 57
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RESULT 7
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                                                                                                                                                                                                                                                                                                              Sequence 29, Application US/08280757B Patent No. 6130316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 1149; DB 3; Best Local Similarity 100.0%; Pred. No. 5.2e-113; Matches 216; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                               APPLICANT: Gray, Gary S.
APPLICANT: Greenfield, Edward
TITLE OF INVENTION: No. 6130316el CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 53
                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         APPLICANT: Freeman, Gordo APPLICANT: Nadler, Lee M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION INFORMATION: AUTHORS: FREEMAN, GOR
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AUTHORS:
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LOCATION:
                                       ZIP:
                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
                                                                                                          STREET:
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                                       02109
                                                                                         Boston
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B7, A New Member Of The 1g Superfamily With
Unique Expression On Activated And Neoplastic B Cells
L: The Journal of Immunology
                                                                        Massachusetts
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                                                                                                          60 State Street, Suite 510
                                                       USA
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                                                                                                                                                                                                                                                                            Gordon J.
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TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/109,393
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: RPTELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400
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OPERATING SYSTEM:
                                     FEATURE:
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                                                                                                                             FEATURE
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DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
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LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
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                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: N-linked glycosylation LOCATION: 19 to 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD: IDENTIFICATION METHOD:
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NAME/KEY:
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                                                                                        NAME/KEY: N-linked glycosylation LOCATION: 152 to 154
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                                                                                                                                                                                    N-linked glycosylation 64 to 66
                                                                                                                                                                                                                                                                            N-linked glycosylation 55 to 57
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N-linked glycosylation
173 to 175
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N: 435
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US-09-159-135-2
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                                                                                                               147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF
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LOCATION:
                                                        207
                                                                                 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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nes 216; Conserva
                                                                                                                                                                                                                                                                                                                                                                                 PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              VOLUME:
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                                                        NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unique Expression On Activated And Neoplastic B Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B7, A New Member Of The Ig Superfamily With
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                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 to 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Journal of Immunology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WHITMAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig C-set domain 105 to 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JEFFREY M.
                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JAMES F.
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Pred. No. 5.2e-113;
                                                                                                                                                                                                                                                                                                 Mismatches
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Sequence 2, Application US/09159135; Patent No. 6149905; GENERAL INFORMATION:

APPLICANT: Ostrand-Rosenberg, Suzai APPLICANT: Baskar, Sivasubramanian

Ostrand-Rosenberg, Suzanne

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TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein

DESCRIPTION: B cell activation antigen; natural ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  NAME/KEY: transmembrane domain LOCATION: 209 to 235 IDENTIFICATION METHOD: similar:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
 NAME KEY:
                                                                                  NAME/KEY: N-linked glycosylation LOCATION: 55 to 57
                                                                                                                                        IDENTIFICATION METHOD: IDENTIFICATION METHOD:
                                              IDENTIFICATION METHOD:
                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                LOCATION: 236 to 254 IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                     NAME/KEY:
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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CITY: Boston
STATE: Massac
                                                                                                                                                                                LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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N-linked glycosylation 64 to 66
                                                                                                                                                                            N-linked glycosylation 19 to 21
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                                                                                                                                                                                                                                                                                 intracellular domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for CD28 T cell surface antigen; transmembrane protein
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                                                               similarity with known
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Best Local Similarity
Matches 216; Conserv
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           181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                        147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206
                                                           121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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                                                                                                                          61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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                                                                                                         87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146
                                                                                                                                                                       27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS: NADLER, LEE M.

TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
                                                                                                                                                                                                                                                                                                                                                               PAGES: 2714-2722
DATE: 15-OCT-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS:
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LOCATION:
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100.0%; Score 1149; DB 4; ilarity 100.0%; Pred. No. 5.2e-113; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                       The Journal of Immunology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WHITMAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FREEDMAN, ARNOLD S. SEGIL, JEFFREY M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FREEMAN, GORDON J.
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105 to 202
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192 to 194
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152 to 154
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: Sequence 19, Application US/08205697A

: Patent No. 6218510
                Patent No. 6294660
GENERAL INFORMATION:
                                                  Sequence 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sharpe, Arlene H.
APPLICANT: Borriello, Francescopaulo
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor
NUMBER OF SEQUENCES: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compation operating SYSTEM: PC-DC SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/205,697A
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                 207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
                                                                                                                                                       181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                      121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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CITY: E
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                                                                                                                                                                                                                                                                              87
                                                                                                                                                                                                                                                                                                                                               27
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                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                      GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86
                                                                                                                                                                                                                                                                                                                                                         GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                                                    ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF
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                                                  Application US/08702525
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Sharpe, Sharpe
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                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1149; DB 4; Length 100.0%; Pred. No. 5.2e-113;
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US-09-450-798-2
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                                                                                                                                                                         Sequence 2, Application US/09450798 Patent No. 6319709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1149; DB 4; Best Local Similarity 100.0%; Pred. No. 5.2e-113; Matches 216; Conservative 0; Mismatches 0;
                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617)227-594
INFORMATION FOR SEQ ID NO:
           APPLICANT: Ostrand-Rosenberg, Suzar APPLICANT: Baskar, Sivasubramanian APPLICANT: Glimcher, Laurie H. APPLICANT: Freeman, Gordon J. APPLICANT: Nadler, Lee M. TITLE OF INVENTION: Tumor Cells Wit
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FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,20
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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LENGTH: 288 amino acid
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TELECOMMUNICATION INFORMATION:
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: LAHIVE & COCKFIELD
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APPLICANT: Nadler, Lee
TITLE OF INVENTION: No. 6294660el Forms of T Ce
TITLE OF INVENTION: Molecules and Uses Therefor
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                             207
                                                                                                                                                                                                                                                                                                                                                                                          147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206
                                                                                                                                                                                                                                                                                                                                                  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMYLIMMSGDMNIWPE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEBLAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
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                                                                                                                             Ostrand-Rosenberg, Suzanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (617)227-7400
(617)227-5941
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                Tumor Cells With Increased Immunogenicity
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TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO:
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IDENTIFICATION METHOD: similari
IDENTIFICATION METHOD: sequence
FEATURE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/450,798
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 03-NOV-1993 ATTORNEY/AGENT INFORMATION:
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NAME/KEY: extracellular domain LOCATION: 1 to 208
IDENTIFICATION METHOD: similar:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
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LENGTH: 288 amino acid
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ADDRESSEE: LAHIVE &
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                             NAME/KEY:
LOCATION:
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TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: intracellular domain LOCATION: 236 to 254 IDENTIFICATION METHOD: similar: IDENTIFICATION METHOD: sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Mandragouras, Amy E
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                                                                                          NAME/KEY: N-linked glycosylation LOCATION: 64 to 66 IDENTIFICATION METHOD: similarit
                  NAME/KEY: N-linked glycosylation LOCATION: 152 to 154 -
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IDENTIFICATION METHOD:
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                                                                                                                                                                                                           N-linked glycosylation
55 to 57
                                                                                                                                                                                                                                                                                                          N-linked glycosylation 19 to 21
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similarity with known
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US-08-403-253A-2 ; Sequence RESULT 12

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Matches
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IDENTIFICATION METHOD:
FEATURE:
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NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
Common Similarit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBLICATION INFORMATION: AUTHORS: FREEMAN, GOR
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              181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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207
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                                                                                                                            87
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                                                                                                                                                                                      Local Similarity
les 216; Conserva
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DATE: 15-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS:
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                                                                               ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
                                                                                                                                            YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                            YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS
NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
                                                             ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF
                                                                                                                                                                                                                                                                                                                                                                                                                                             3: WHITMAN, JAMES F.
3: NADLER, LEE M.
B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells
                                                                                                                                                                                                                                                                                                                                                                                                                 143
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                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               The Journal of Immunology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEE, GRACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FREEMAN, GORDON J.
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1 to 104
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                                                                                                                                                                                                                                                      100.0%; Score 1149; DB 4; 100.0%; Pred. No. 5.2e-113; tive 0; Mismatches 0;
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Patent No. 6352694 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
APPLICANT: Gray, Gary S., Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400 TELEFAX: (617) 742-4214
                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
DESCRIPTION:
                                                             FEATURE
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                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/864,805 FILING DATE: 7 APR 1992 APPLICATION NUMBER: US 08/247,505 FILING DATE: 23 MAY 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 3 JUNE 1994 APPLICATION NUMBER: US 0
NAME/KEY: transmembrar
LOCATION: 209 to 235
IDENTIFICATION METHOD:
                                                                           NAME/KEY: extracellular domain LOCATION: 1 to 208 IDENTIFICATION METHOD: similari IDENTIFICATION METHOD: sequence
                                                                                                                                                                          OTHER INFORMATION:
                                                                                                                                                                                        NAME/KEY: signal sequence LOCATION: -34 to -1 IDENTIFICATION METHOD: ami
                                                                                                                                                                                                                                                                               NLECULE TYPE: protein

DESCRIPTION: B cell activation antigen; natural ligand

DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
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similarity with known
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                                                                                           similarity with known
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                                                                           sequence
                   US-08-403-253A-2
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VOLUME:
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LOCATION:
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DATE: 15-OCT-1989
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AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
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IDENTIFICATION METHOD:
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RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION METHOD:
                                                                                                                                                                                   FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
                                                                                  The Journal of Immunology
                                                                                                                                                     WHITMAN, JAMES F.
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192 to 194
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152 to 154
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RESULT 13
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APPLICANT:
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Best Local Similarity
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Best Local
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                                                                                            Matches 216;
                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: UZLUZ V. COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,20
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APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
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                                                                                                            Local Similarity
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                                               GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
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YKNRTIFDITNNISTVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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                                GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86
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                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Pa
SEQ ID NO 131
LENGTH: 473
                                                                                         Sequence 36, Application US/09460384 Patent No. 6337316 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 131, Application US/09171945
Patent No. 6277599
GENERAL INFORMATION:
APPLICANT: Emery, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-17
PRIOR FILING DATE: 1996-05-04
PRIOR PRIOR APPLICATION NUMBER: PCT/GB97/011
PRIOR PILING DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System FILE REFERENCE: Monoclonal Antibody to CEA CURRENT APPLICATION NUMBER: US/09/171,945
CURRENT FILING DATE: 1998-10-29
CURRENT FILING DATE: 1998-10-29
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APPLICANT:
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIIVWQKEKKMVLIMMSGDMNIWPE 60
                APPLICANT: EL TAYAR, Nabil
BLECHNER, Steve
JAMESON, Brad
TEPPER, Mark
TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
INVENTION: CD28/CTLA-4 INHIBITING PEPTIDOMIMETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1149; DB 4; 100.0%; Pred. No. 1.1e-112;
                                                      Steven
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-460-384-36
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Search completed: June 18, 2002, 11:43:29 Job time: 22 sec
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FILING DATE: 11-JUN-1998
APPLICATION NUMBER: US 60/049,470
FILING DATE: 12-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: EL TAYAR-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEPHONE: (202) 737-3528
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 95.9%; Score 1102; DB 4; Length 208; Best Local Similarity 100.0%; Pred. No. 2.8e-108; Matches 208; Conservative 0; Mismatches 0; Indels
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APPLICATION NUMBER: US/09/460,384
FILING DATE: 13-Dec-1999
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Ste. 300
                                                                                                                                                                                               SNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSF 188
                                                                                                                                                                                                                                                      ITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPŚISDFEIPT 128
                                                                                                                                      MCLIKYGHLRVNOTFNWNTTKQEHFPDN 216
                                                                                                                                                                            SNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSF 180
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                                                                                              HCLIKYGHLRVNQTFNWNTTKQEHFPDN 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 208 amino acids TYPE: amino acid
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